

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 06:11:13 ; Search time 4270.53 Seconds
(without alignments)
13027.239 Million cell updates/sec

Title: US-10-054-680-3
Perfect score: 1863
Sequence: 1 atggcgtgggttaaggttgca.....ggaaagccagtattgggtga 1863

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB		ID	Description
No.	Score	Match	Length	DB	ID			
1	1784.4	95.8	1788	29	AY401283		AY401283	Homo sapi
2	1783	95.7	3186	11	BC036783		BC036783	Homo sapi
3	1739.4	93.4	1788	29	AY401284		AY401284	Pan trogl
4	1544.4	82.9	1788	29	AY401285		AY401285	Mus muscu
5	1521	81.6	2534	11	AK044636		AK044636	Mus muscu
6	971	52.1	1589	11	CNSLT1IBJ		BX248763	human ful
7	899.6	48.3	941	13	BX374548		BX374548	BX374548
8	805	43.2	887	12	BI913344		BI913344	603178823
9	784.8	42.1	2922	29	AY398961		AY398961	Homo sapi
10	768.2	41.2	939	13	BX347210		BX347210	BX347210
11	755	40.5	2922	29	AY398963		AY398963	Mus muscu
12	739.8	39.7	792	12	BI522813		BI522813	603175911
13	737.8	39.6	920	13	BX368185		BX368185	BX368185
14	710.4	38.1	4374	11	AK035163		AK035163	Mus muscu
15	708.4	38.0	922	13	BX390204		BX390204	BX390204
16	673.2	36.1	775	13	BQ770745		BQ770745	UI-M-FI0-
17	638	34.2	3573	11	AK048160		AK048160	Mus muscu
18	635.4	34.1	2516	29	AY408693		AY408693	Homo sapi
19	607	32.6	2881	29	AY398962		AY398962	Pan trogl
20	598.6	32.1	971	13	BX368184		BX368184	BX368184
21	574.6	30.8	752	14	CF532853		CF532853	UI-M-GH0-
c 22	553.6	29.7	1062	29	CNS04DXR		AL286344	Tetraodon
23	503.8	27.0	588	14	CF533347		CF533347	UI-M-FY0-
24	497	26.7	704	14	CF729293		CF729293	UI-M-HD0-
25	483.2	25.9	854	13	BX325851		BX325851	BX325851
26	456.8	24.5	676	10	BB280958		BB280958	BB280958
27	412.4	22.1	503	28	BZ211245		BZ211245	CH230-426
c 28	407.4	21.9	499	28	BH349372		BH349372	CH230-32M
29	403.4	21.7	2515	29	AY408695		AY408695	Mus muscu
30	397.2	21.3	911	13	BU901346		BU901346	AGENCOURT
31	368.4	19.8	1201	13	BX355386		BX355386	BX355386
32	363.6	19.5	829	29	CC501501		CC501501	CH240_339
33	359	19.3	569	12	BI906774		BI906774	603064517
34	352	18.9	741	14	CF539360		CF539360	UI-M-GH0-
35	341.2	18.3	830	13	BU747974		BU747974	CH3#016_H
c 36	339.4	18.2	833	13	BU747973		BU747973	CH3#016_H
c 37	338	18.1	1020	29	CNS03Y28		AL265769	Tetraodon
38	327.4	17.6	2472	29	AY408694		AY408694	Pan trogl
c 39	320	17.2	384	28	AZ258968		AZ258968	RPCI-23-1
c 40	304.4	16.3	818	28	BZ163286		BZ163286	CH230-276
41	303	16.3	462	9	AL712986		AL712986	DKFZp686J
42	295.8	15.9	693	10	BB648018		BB648018	BB648018
c 43	294.2	15.8	551	29	FR0052027		AL688306	Fugu rubr
44	289.8	15.6	712	13	BY732330		BY732330	BY732330
45	285.6	15.3	900	14	CF265737		CF265737	AGENCOURT

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RESULT 1
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LOCUS      AY401283                1788 bp    DNA        linear    GSS 15-DEC-2003
DEFINITION Homo sapiens SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION  AY401283
VERSION    AY401283.1  GI:39757272
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 1788)
  AUTHORS  Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE    Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED    14671302
REFERENCE  2  (bases 1 to 1788)
  AUTHORS  Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE    Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT    This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
     source      1. .1788
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                  /mol_type="genomic DNA"
                  /db_xref="taxon:9606"
     gene        <1. .>1788
                  /gene="SLC8A3"
                  /locus_tag="HCM0839"
ORIGIN
     Query Match      95.8%;   Score 1784.4;   DB 29;   Length 1788;
     Best Local Similarity  99.9%;   Pred. No. 0;
     Matches 1785;   Conservative    0;   Mismatches    1;   Indels    0;   Gaps    0;

Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTGGGCTGGTTACC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTGGGCTGGTTACC 60

Qy      61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

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Qy	121	ACAGGGCAGAACAATGAGTCCTGTTACAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTACAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACTTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCTTATGGCC	420
Db	361	ACCAGCACAACTTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCTTATGGCC	420
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
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Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
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Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
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Qy	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
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Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTAT	1786
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTAT	1786

RESULT 2
 BC036783
 LOCUS BC036783 3186 bp mRNA linear HTC 19-NOV-2003
 DEFINITION Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3, mRNA (cDNA clone IMAGE:5732743), with apparent retained intron.
 ACCESSION BC036783
 VERSION BC036783.1 GI:23331089
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3186)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 3186)
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (23-AUG-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 79 Row: j Column: 21
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 17865803
 This clone has the following problem: retained intron.

FEATURES	Location/Qualifiers
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	/clone_lib="NIH MGC_124"
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	/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 95.7%; Score 1783; DB 11; Length 3186;
 Best Local Similarity 98.4%; Pred. No. 0;
 Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
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Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	618	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	677
Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	678	ACAGGGCAGAACAAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	737
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	738	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAG	797
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	798	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	857
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	858	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	917
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
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Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
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Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
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Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1458	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1517
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1518	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1577
Qy	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1578	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1637
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Db	1638	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1697
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1698	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1757
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1758	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1817
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320

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Db      1878 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1937
Qy      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db      1938 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1997
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Db      1998 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 2057
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Db      2058 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 2117
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Db      2238 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2297
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RESULT 3

AY401284

LOCUS AY401284 1788 bp DNA linear GSS 15-DEC-2003

DEFINITION Pan troglodytes SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY401284

VERSION AY401284.1 GI:39757273

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 1788)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1788)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
 FEATURES Location/Qualifiers
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 /mol_type="genomic DNA"
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 gene <1..>1788
 /gene="SLC8A3"
 /locus_tag="HCM0839"
 ORIGIN

 Query Match 93.4%; Score 1739.4; DB 29; Length 1788;
 Best Local Similarity 97.8%; Pred. No. 0;
 Matches 1746; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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 Qy 421 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

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Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
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Db	781	ATGCACAAAAAGTACCGCACAGATAAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
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Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCTAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGGATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGANNGAGGTGCACACCGATGANNCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
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Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320

Db 1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTNNNGCC 1320

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Db 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db 1381 CAGAAGGAGTTCTCCGTAGGCATAATTNNNGACGACATTTNNNAGGAGGATGAACACTTN 1440

Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db 1441 NNNNNAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGNCTCCA 1500

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Db 1501 GCAATANNCAACAGTNNNNCCTTGCCTCGGGCTGTNNTAGCCTCCCCTTGTGTNGCCACA 1560

Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620
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Db 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620

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Db 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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Db 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 1786

RESULT 4

AY401285

LOCUS AY401285 1788 bp DNA linear GSS 15-DEC-2003

DEFINITION Mus musculus SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY401285

VERSION AY401285.1 GI:39757274

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1788)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1788)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

	Location/Qualifiers
source	1..1788
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gene	<1..>1788
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ORIGIN

Query Match 82.9%; Score 1544.4; DB 29; Length 1788;
Best Local Similarity 91.5%; Pred. No. 0;
Matches 1635; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

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Db	61	TTTGTGCTCTTCCTGAATGTCTTCGAGCAGAGGCTGGTGAATCGGGGATGTGCCCAAGT	120
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Db	121	GCAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCAGACTGCAAGGAGGGTGTCTATTTG	180
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Qy	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
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Db	301	TCTATTGAAGTCATTACTTCCCAAGAGAGGGAAGTGACCATCAAGAAGCCCAATGGAGAG	360
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
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Db	421	CTGGGCTCTTCTGCTCCAGAGATTCTCCTGTCTTTAATTGAGGTGTGTGGTCACGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540

Db	481	ATTGCTGGTGATCTGGGACCATCTACCATCGTTGGCAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
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Db	601	CGAGTCTTCTTCGTACGGCTGCTTGGAGCATCTTCGCCTACATTTGGCTCTATATGATC	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCTCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTTACTCTCTTCTTC	720
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Db	721	TTTCCCGTGTGTGTCCTGCTGGCTTGGGTGGCAGATAAGCGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAATACCGCACAGATAAACACCGAGGAATTATCATTGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCTCACTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	TTTACACCTTTGGAAGGAAAGGAGGTAGATGAATCTCGCAGGGAAATGATCCGGATTCTA	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAACAAAACACCCAGAAAAGGACCTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCCATCAACAGAAGAGCCGTGCTTCTACCGCATCCAAGCCACCCGG	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACCAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATACTTAAGAAGCATGCAGCCGAGCAAGCCAAGAAGACC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCATACCGATGAGCCGAGGACTTTGCCTCTAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTATCAGTGCCTGGAGAACTGTGGAGCTGTCTCCTGACCGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGATATATCCAAGACCATGTACGTGGACTACAAAACAGAGGACGGCTCCGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCAGACTATGAGTTCACAGAGGGCACTGTGGTTCTGAAGCCAGGAGAGACC	1380

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 Db 1681 ACAGTCATCGTCCCTTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGTGGCGAGGACTTT 1740

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAACTGTAT 1786
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 Db 1741 GAAGATGCATATGGGGAGCTGGAGTTCAAGAATGATGAAACAGTGT 1786

RESULT 5

AK044636

LOCUS AK044636 2534 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930029A02 product:solute carrier family 8 (sodium/calcium exchanger), member 3, full insert sequence.

ACCESSION AK044636

VERSION AK044636.1 GI:26336660

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2534)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

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            /translation="MCPVQGRMTSPVRGHQTARRVSFCQLWYPENPSLGDKIARVIVY
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            IKHLRVFFVTAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKR
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            RREMIRILKDLKQKHPEKDLQVEMANYALSHQQKSRAFYRIQATRMMTGAGNILK
            KHAAEQAKKTSSMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLLTVVRKGGDISKT
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            VRVEEQQLAEGMLPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSES
            IGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDAYGELEFKNDET VKTIRVKI
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ORIGIN

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Query Match      81.6%;  Score 1521;  DB 11;  Length 2534;
Best Local Similarity  90.2%;  Pred. No. 0;
Matches 1662;  Conservative  0;  Mismatches 175;  Indels  6;  Gaps  3;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGG-CTGGTTAC  59
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Db      603 ATGGCGTGGTTACGGCTGCACCCTCTCACCTCTGCCTTCCTCCATCTTGGGCCTGGTTAC  662

Qy      60 CTTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAG  119
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      663 TTTTGTGCTCTTCCTGAATTGTCTTCGAGCAGAGGCTGGTGACTCGGGGGATGTGCCAG  722

Qy      120 CACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCT  179
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Db      723 TGCAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCAGACTGCAAGGAGGGTGTCATTTT  782

Qy      180 GCCAA-TCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCT  238
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Db      783 GCCAACTCTGGTATCCAGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCT  842

Qy      239 ATTTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGG  298
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Db      843 ATTTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGATTTCATGG  902

Qy      299 CATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAG  358

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Db	903	CATCTATTGAAGTCATTACTTCCCAAGAGAGGGAAGTGACCATCAAGAAGCCCAATGGAG	962
Qy	359	AAACCAGCACAAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGG	418
Db	963	AGACCAGCACAACTACAATTTCGGGTATGGAATGAACTGTCTCCAATCTGACCCTGATGG	1022
Qy	419	CCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGT	478
Db	1023	CCCTGGGCTCTTCTGCTCCAGAGATTCTCCTGTCTTTAATTGAGGTGTGTGGTCACGGGT	1082
Qy	479	TCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCA	538
Db	1083	TCATTGCTGGTGATCTGGGACCATCTACCATCGTTGGCAGTGCAGCCTTCAACATGTTCA	1142
Qy	539	TCATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATC	598
Db	1143	TCATCATTGGCATCTGTGTCTATGTGATCCAGATGGGGAGACTCGAAAGATCAAGCACC	1202
Qy	599	TACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGA	658
Db	1203	TGCGAGTCTTCTTCGTCACGGCTGCTTGGAGCATCTTCGCCTACATTTGGCTCTATATGA	1262
Qy	659	TTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCT	718
Db	1263	TCCTGGCAGTCTTCTCTCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTTACTCTCTTCT	1322
Qy	719	TCTTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAAT	778
Db	1323	TCTTTCCCGTGTGTGTCTGCTGGCTTGGGTGGCAGATAAGCGACTGCTCTTCTACAAAT	1382
Qy	779	ACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTG	838
Db	1383	ACATGCACAAAAAATACCGCACAGATAAACACCGAGGAATTATCATTGAGACAGAGGGTG	1442
Qy	839	ACCACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGA	898
Db	1443	ACCACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCTCACTTTCTAGATGGGA	1502
Qy	899	ACCTGGTGCCCCCTGGAAGGGAAGGAAGTGATGAGTCCCGCAGAGAGATGATCCGGATTC	958
Db	1503	ACTTTACACCTTTGGAAGGAAAGGAGGTAGATGAATCTCGCAGGGAAATGATCCGGATTC	1562
Qy	959	TCAAGGATCTGAAGCAAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCA	1018
Db	1563	TAAAGGATCTGAAACAAAAACACCCAGAAAAGGACCTAGATCAGCTGGTGGAGATGGCCA	1622
Qy	1019	ATTACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTC	1078
Db	1623	ATTACTATGCTCTTTCCCATCAACAGAAGAGCCGTGCTTTCTACCGCATCCAAGCCACCC	1682
Qy	1079	GTATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGG	1138
Db	1683	GGATGATGACTGGTGCGGGCAATATACTTAAGAAGCATGCAGCCGAGCAAGCCAAGAAGA	1742
Qy	1139	CCTCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCT	1198

Db 1743 CCTCCAGCATGAGCGAGGTGCATACCGATGAGCCGGAGGACTTTGCCTCTAAGGTCTTCT 1802

Qy 1199 TTGACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGA 1258
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Db 1803 TTGACCCATGTTCTTATCAGTGCCTGGAGAACTGTGGAGCTGTCTCCTGACCGTGGTGA 1862

Qy 1259 GGAAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTG 1318
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Db 1863 GGAAAGGGGGAGATATATCCAAGACCATGTACGTGGACTACAAAACAGAGGACGGCTCCG 1922

Qy 1319 CCAATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGA 1378
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Db 1923 CCAATGCAGGGGCAGACTATGAGTTCACAGAGGGCACTGTGGTTCTGAAGCCAGGAGAGA 1982

Qy 1379 CCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACT 1438
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Db 1983 CCCAGAAGGAGTTCTCTGTGGGCATCATTGATGATGACATTTTTGAGGAGGATGAACACT 2042

Qy 1439 TCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTC 1498
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Db 2043 TCTTTGTGAGGCTGAGCAATGTCCGTGTAGAAGAGGAGCAGCTGGCGGAGGGGATGCTCC 2102

Qy 1499 CAGCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCA 1558
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Db 2103 CAGCAATACTCAATAGTCTTCCCTTGCCTCGGGCTGTCTGGCCTCCCCTTGTGTGGCCA 2162

Qy 1559 CAGTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTC 1618
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Db 2163 CAGTAACCATCTTGGATGATGACCATGCAGGAATTTTCACTTTTGAATGTGATAACCATTC 2222

Qy 1619 ATGTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGG 1678
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Db 2223 ATGTCAGTGAAAGTATTGGTGTTATGGAAGTCAAGGTTTTGAGGACATCAGGTGCCAGGG 2282

Qy 1679 GTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACT 1738
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Db 2283 GCACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGTGGCGAGGACT 2342

Qy 1739 TTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGG 1798
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Db 2343 TTGAAGATGCATATGGGGAGCTGGAGTTCAAGAATGATGAAAC----AGTGAAAACCATA 2398

Qy 1799 AAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db 2399 AGGGTTAAATAGTAGATGAGGAGGAGTACGAGAGGCAAGAGA 2441

RESULT 6

CNSLT1IBJ

LOCUS CNSLT1IBJ 1589 bp mRNA linear HTC 18-JUN-2003

DEFINITION human full-length cDNA 5-PRIME end of clone CS0DB006YD18 of Neuroblastoma of Homo sapiens (human).

ACCESSION BX248763

VERSION BX248763.1 GI:28375580

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1589)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue

REFERENCE 2 (bases 1 to 1589)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (13-FEB-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES Location/Qualifiers
source 1. .1589
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DB006YD18"
/tissue_type="Neuroblastoma"
/note="end : 5-PRIME~Cot 10-normalized~vector pCMVSPORT_6"
CDS 619. .>1589
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD66570.1"
/db_xref="GI:28375581"
/translation="MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQN
NESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASI
EVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGF
IAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKHKLRLVFFITAAWSIFAYIWLY
MILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIE
TEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDL"

ORIGIN

Query Match 52.1%; Score 971; DB 11; Length 1589;
Best Local Similarity 100.0%; Pred. No. 2.7e-274;
Matches 971; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db 619 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 678

Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
|||||

Db 679 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 738

Qy 121 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG 180
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Db 739 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG 798

Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	799	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	858
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	859	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	918
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	919	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	978
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	979	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	1038
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	1039	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	1098
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1099	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1158
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	1159	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	1218
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	1219	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1278
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1279	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1338
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1339	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1398
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1399	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1458
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1459	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1518
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1519	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1578
Qy	961	AAGGATCTGAA	971
Db	1579	AAGGATCTGAA	1589

BX374548

DEFINITION BX374548 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens cDNA clone CS0DB006YD18 5-PRIME, mRNA sequence.

ACCESSION BX374548

VERSION BX374548.1 GI:30438490

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 941)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7256.r For more information about this cluster, see

<http://www.genoscope.cns.fr/>

```
cgi-bin/cluster.cgi?seq=CS0DB006DB09 DB1287 2&cluster=7256.r.
```

Contact : Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DB006DB09 DB1287 2.

FEATURES

source

Location/Qualifiers

1. .941

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/organism="Homo sapiens"
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/mol type="mRNA"
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/db xref="taxon:9606"
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/clone="CS0DB006YD18"
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/tissue type="NEUROBLASTOMA COT 10-NORMALIZED"
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/clone lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 48.3%; Score 899.6; DB 13; Length 941;

Best Local Similarity 97.7%; Pred. No. 2.2e-253;

Matches 919; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

Qy 685 GTCCAGGTTTGGGAAGGCCCTCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCC 744

Db 1 GGCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCC-GTGTGTGTCCTTCTGGCC 59

QY 745 TGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGAC 804

Db 60 TGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGAC 119

Qy 805 AAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGAT 864

Db 120 AAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGAT 179

Qy	865	GGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAGGAA	924
Db	180	GGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAGGAA	239
Qy	925	GTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCA	984
Db	240	GTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCA	299
Qy	985	GAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAG	1044
Db	300	GAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAG	359
Qy	1045	AAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATC	1104
Db	360	AAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATC	419
Qy	1105	CTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACC	1164
Db	420	CTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACC	479
Qy	1165	GATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTG	1224
Db	480	GATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTG	539
Qy	1225	GAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGAGACATGTCAAAGACC	1284
Db	540	GAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGAGACATGTCAAAGACC	599
Qy	1285	ATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTC	1344
Db	600	ATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTC	659
Qy	1345	ACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATA	1404
Db	660	ACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATA	719
Qy	1405	ATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGC	1464
Db	720	ATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGNTAGGTTGAGCAATGTCCGC	779
Qy	1465	ATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTC AACAGTCTTCCTTG	1524
Db	780	ATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTNNCAGCATATTCAAACAGTCTTCCTTG	839
Qy	1525	CCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGATGATGACCAT	1584
Db	840	CCTCGGGCTGTCCTAGCCTNCCCTTGNGTGGNCACAGTTACCATCTTGATGATGACCAT	899
Qy	1585	GCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAG	1625
Db	900	GCNAGCATCTTCACTTTTGAATGTGATACTATTCATGTCAG	940

RESULT 8

BI913344

LOCUS

BI913344

887 bp

mRNA

linear

EST 16-OCT-2001

DEFINITION 603178823F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5243308 5', mRNA sequence.
 ACCESSION BI913344
 VERSION BI913344.1 GI:16177710
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 887)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM11613 row: m column: 05
 High quality sequence stop: 782.
 FEATURES
 source Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5243308"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_121"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."
 ORIGIN
 Query Match 43.2%; Score 805; DB 12; Length 887;
 Best Local Similarity 98.0%; Pred. No. 1.8e-225;
 Matches 836; Conservative 0; Mismatches 15; Indels 2; Gaps 2;
 Qy 916 GGG AAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAA 975
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 Db 1 GGG AAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAA 60
 Qy 976 AAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCC 1035
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 Db 61 AAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCC 120
 Qy 1036 CACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCA 1095


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ACCESSION      AY398961
VERSION        AY398961.1   GI:39754950
KEYWORDS       GSS.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1   (bases 1 to 2922)
AUTHORS        Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
                Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
                Adams,M.D. and Cargill,M.
TITLE          Inferring nonneutral evolution from human-chimp-mouse orthologous
                gene trios
JOURNAL        Science 302 (5652), 1960-1963 (2003)
PUBMED         14671302
REFERENCE      2   (bases 1 to 2922)
AUTHORS        Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
                Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
                Adams,M.D. and Cargill,M.
TITLE          Direct Submission
JOURNAL        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                Rockville, MD 20850, USA
COMMENT        This sequence was made by sequencing genomic exons and ordering
                them based on alignment.
FEATURES
    source      Location/Qualifiers
                1. .2922
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
    gene        <1. .>2922
                /gene="SLC8A1"
                /locus_tag="HCM0065"

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Qy	409	ACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT	468									
Db	412	ACCTTGATGGCCCTGGGATCTTCTGCTCCTGAGATTCTCCTTTCAGTAATTGAAGTGTGT	471									
Qy	469	GGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTC	528									
Db	472	GGCCATAACTTCACTGCAGGAGACCTCGGTCTAGCACCATCGTGGGAAGTGTGCATTC	531									
Qy	529	AACATGTTTCATCATCATTTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAG	588									
Db	532	AATATGTTTCATCATTTATTCGACTCTGTGTTTATGTGGTGCCTGACGGAGAGACAAGGAAG	591									
Qy	589	ATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGG	648									
Db	592	ATTAAGCATTTCGCTGTCTTCTTTGTGACAGCAGCCTGGAGCATCTTTGCCTACACCTGG	651									
Qy	649	CTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTC	708									
Db	652	CTTTACATTATTTTGTCTGTATATCTCCTGGTGTGTGGAGGTCTGGGAAGGTTTGCTT	711									
Qy	709	ACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTC	768									
Db	712	ACTTTCTTCTTCTTTCCCATCTGTGTTGTGTTGCTTGGGTAGCGGATAGGAGACTTCTG	771									
Qy	769	TTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAG	828									
Db	772	TTTTACAAGTATGTCTACAAGAGGTATCGAGCTGGCAAGCAGAGGGGGATGATTATTGAA	831									
Qy	829	ACAGAGGGTGACCACCC-----TAAGGGCATTGAGATGGATGGGAAAATGATGAAT	879									
Db	832	CATGAAGGAGACAGGCCATCTTCTAAGACTGAAATTGAAATGGACGGGAAAGTGGTCAAT	891									
Qy	880	TCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAG-----	921									
Db	892	TCTCATGTTGAAAATTTCTTAGATGGTGCTCTGGTTCTGGAGGTGGATGAGAGGGACCAA	951									
Qy	922	GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACAC	981									
Db	952	GATGATGAAGAAGCTAGGCGAGAAATGGCTAGGATTCTGAAGGAACCTAAGCAGAAGCAT	1011									
Qy	982	CCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCACCAA	1041									
Db	1012	CCAGATAAAGAAATAGAGCAATTAATAGAATTAGCTAACTACCAAGTCCTAAGTCAGCAG	1071									
Qy	1042	CAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAAT	1101									
Db	1072	CAAAAAGTAGAGCATTTTATCGCATTCAAGCTACTCGCCTCATGACTGGAGCTGGCAAC	1131									
Qy	1102	ATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCAC	1161									
Db	1132	ATTTTAAAGAGGCATGCAGCTGACCAAGCAAGGAAGGCTGTCAGCATGCACGAGGTCAAC	1191									
Qy	1162	ACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG	1218									

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7256.r For
more information about this cluster, see
[http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAA004ZB09_CS00355_1&cluster=7256.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAA004ZB09_CS00355_1&cluster=7256.r).
Contact : Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAA004ZB09_CS00355_1.

FEATURES Location/Qualifiers
source 1. .939
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DB006YD18"
/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 41.2%; Score 768.2; DB 13; Length 939;
Best Local Similarity 95.6%; Pred. No. 1.4e-214;
Matches 854; Conservative 0; Mismatches 33; Indels 6; Gaps 6;

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Qy      105 AGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAA 164
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Db      22 AGGGGACGTGCC-AGCACAGGGCAGAACAATGAGTCCTGTT-AGGGTCATCGGACTGCAA 79

Qy      165 GGAGGGTGTTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGC 224
          |||||
Db      80 GGAGGGTGTTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGC 139

Qy      225 CAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGC 284
          |||||
Db      140 CAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGC 199

Qy      285 TGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAA 344
          |||||
Db      200 TGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAA 259

Qy      345 GAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAACTGTCTCCAA 404
          |||||
Db      260 GAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAACTGTCTCCAA 319

Qy      405 CCTGACCCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTAATTGAGGT 464
          |||||
Db      320 CCTGACCCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTAATTGAGGT 379

Qy      465 GTGTGGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGC 524

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      |||
Db      380 GTGTGGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTTGTAGGGAGTGCAGC 439
Qy      525 CTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCG 584
      |||
Db      440 CTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCG 499
Qy      585 CAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACAT 644
      |||
Db      500 CAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACAT 559
Qy      645 CTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCT 704
      |||
Db      560 CTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGG-AGGCCT 618
Qy      705 CCTCACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACT 764
      |||
Db      619 CCTCACTCTCTTCTTCTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACT 677
Qy      765 GCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCAT 824
      |||
Db      678 GCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGGATTATAT 737
Qy      825 AGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCA 884
      |||
Db      738 AGAGACAGAGGGTGACCACCCTAGGGGCTTTGGGATGGGTGGGAAAAGGATGAATTCCCA 797
Qy      885 TTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGT-CCCGCAGAG 943
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Db      798 TTTTCTAGGAGGGAAACCTGTGCCCCCTGAAGGGAAGAAAGTGGATTAATCCCCGAGAG 857
Qy      944 AGATGATCCGGATTCTC-AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTT 995
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Db      858 AGATGAACCCGGTTCTCTAGGGATCTGAAACCAAAAACCCCCAAAAAGGCCT 910

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RESULT 11

AY398963

LOCUS AY398963 2922 bp DNA linear GSS 15-DEC-2003

DEFINITION Mus musculus SLC8A1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY398963

VERSION AY398963.1 GI:39754952

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2922)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2922)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1..2922
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
gene <1..>2922
/gene="SLC8A1"
/locus_tag="HCM0065"

ORIGIN

Query Match 40.5%; Score 755; DB 29; Length 2922;
Best Local Similarity 67.8%; Pred. No. 2.3e-210;
Matches 1134; Conservative 0; Mismatches 500; Indels 39; Gaps 4;

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Qy      142  TGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTGCCAATCTGGTACCCGGAGAAC 201
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Db      145  TGTACTGGCTCATATTACTGTAAGAAAGGGGTGATCTTGCCCATTTGGGAACCCCAAGAC 204

Qy      202  CCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATG 261
      || || ||||| ||||| || | | ||| ||||| || | |||||
Db      205  CCATCTTTTGGGGACAAAATTGCTAGAGCAACTGTGTATTTTGTGGCCATGGTCTACATG 264

Qy      262  TTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCT 321
      ||||| || || || |||| |||| || || | |||| || |||||
Db      265  TTCCTTGGAGTTTCTATTATTGCAGACCGGTTTATGTCTCTATAGAGGTCATCACCTCT 324

Qy      322  CAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCCTATTCGG 381
      ||||| || | || || ||||| ||||| |||| || || || | |
Db      325  CAAGAGAAAGAAATAACGATAAAGAAACCGAATGGAGAGACCACCAAGACGACGGTGAGA 384

Qy      382  GTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAG 441
      ||||| || |||| || ||||| || ||||| || ||||| || |||||
Db      385  ATCTGGAACGAGACTGTGTGCAACCTGACCTTGATGGCCCTGGGATCTTCTGCTCCTGAG 444

Qy      442  ATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCT 501
      || |||| || | |||| |||| || || | ||| || || || |||| ||
Db      445  ATTCTCCTGTCTAGTCATTGAAGTGTGCGGCCATAACTTCACCGCAGGGGACCTGGGTCCC 504

Qy      502  TCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTAC 561
      |||| || || |||| |||| ||||| ||||| || | ||||| |||
Db      505  AGCACCATCGTGGGAAGTGCTGCCTTTAACATGTTTCATCATAATCGCACTCTGTGTTTAC 564

Qy      562  GTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCT 621
      |||| || ||||| || ||||| ||||| || || |||| | || ||
Db      565  GTGGTCCCTGATGGAGAGACAAGGAAGATCAAGCATCTGCGTGTGTTCTTTGTGACAGCA 624

Qy      622  GCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGT 681

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Db	625	GCCTGGAGCATCTTTGCCTATACCTGGCTTTATATAATCTTGTCTGTCTCAGCTCTCCTGGA	684
Qy	682	GTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTCCAGTGTGTGTCTCTCTG	741
Db	685	GTTGTGGAGGTCTGGGAAGGCTTGCTTACTTTCTTCTTCTTCCCATCTGCGTTGTGTTC	744
Qy	742	GCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACA	801
Db	745	GCGTGGGTAGCAGACAGGCGGCTTCTCTTTTACAAGTATGTCTACAAGCGGTACAGGGCC	804
Qy	802	GACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCC-----TAAGGGC	852
Db	805	GGCAAGCAGAGGGGGATGATCATTGAACATGAAGGAGACAGACCAGCTTCCAAAAGTGA	864
Qy	853	ATTGAGATGGATGGGAAAATGATGAATCCCATTTTCTAGATGGGAACCTGGTGCCCCCTG	912
Db	865	ATCGAAATGGATGGGAAAGTGGTCAACTCTCATGTTGACAATTTCTTAGATGGGGCTCTG	924
Qy	913	G-----AAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGG	954
Db	925	GTTTTGGAAGTTGATGAGAGGGACCAAGATGATGAGGAAGCCAGGCGTGAGATGGCAAGG	984
Qy	955	ATTCTCAAGGATCTGAAGCAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATG	1014
Db	985	ATTCTGAAGGAAGTTAAGCAGAAGCATCCTGAGAAAGAAATTGAGCAATTAATAGAATTA	1044
Qy	1015	GCCAATTACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCC	1074
Db	1045	GCCAACTACCAGGTCTAAGTCAACAGCAGAAAAGCCGAGCATTTTACAGGATTCAAGCT	1104
Qy	1075	ACTCGTATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACCAAGCCAAG	1134
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Qy	1135	AAGGCCTCCAGCATGAGCGAGGTGCACACCGATGAGCCTG---AGGACTTTATTTCCAAG	1191
Db	1165	AAGGCTGTCTAGTATGCATGAAGTCAACATGGAAATGGCTGAAAACGACCCAGTCAGTAAG	1224
Qy	1192	GTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCTTGACA	1251
Db	1225	ATCTTCTTTGAGCAAGGAACATAACCAGTGTCTAGAGAAGTGTGGTACTGTGGCCCTCACC	1284
Qy	1252	GTGGTGAGGAAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGAT	1311
Db	1285	ATTATGCGCAGAGGGGGCGACTTGAGCACCCTGTGTTTGTGACTTCAGGACAGAAGAC	1344
Qy	1312	GGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCA	1371
Db	1345	GGCACAGCCAATGCTGGGTCTGATTATGAATTCACGGAAGGGACTGTGATCTTCAAACCA	1404
Qy	1372	GGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGAT	1431
Db	1405	GGGGAGACCCAGAAGGAAATCAGAGTTGGCATCATTGATGATGATATCTTTGAAGAAGAT	1464
Qy	1432	GAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGG	1491

Db 1465 GAAAACTTCCTTGTGCATCTTAGCAATGTCAGAGTCTCTTCAGATGTTTCAGAAGATGGC 1524

Qy 1492 ATGCCTCCAGCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGT 1551
 || | | | | | | | | | | | | | | | |

Db 1525 AT-----ACTAGAATCCAATCACGTTCTTCAATTGCTTGTCTTGGGTCACCCAGC 1575

Qy 1552 GTGGCCACAGTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGAT 1611
 |||| | |||| | | ||||| | | | | | | | | | | | | | | | | |

Db 1576 ACTGCCACCATAACCATTTTTGATGATGACCATGCAGGCATCTTACATTTGAGGAACCC 1635

Qy 1612 ACTATTCATGTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGT 1671
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Db 1636 GTGACTCACGTGAGCGAGAGCATTTGGCATCATGGAGGTGAAGGTTTGAAGACCTCTGGA 1695

Qy 1672 GCCCCGGGTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGT 1731
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Db 1696 GCTCGAGGAAATGTTATCATTTCCCTACAAAATATTGAAGGCACAGCCCCGAGGTGGAGGG 1755

Qy 1732 GAGGACTTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1784
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Db 1756 GAAGACTTTGAGGACACCTGTGGAGAGCTCGAATTCCAGAACGATGAAATAGT 1808

RESULT 12

BI522813

LOCUS BI522813 792 bp mRNA linear EST 29-AUG-2001

DEFINITION 603175911F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240066 5', mRNA sequence.

ACCESSION BI522813

VERSION BI522813.1 GI:15347605

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 792)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11605 row: f column: 03

High quality sequence stop: 778.

FEATURES

source

Location/Qualifiers

1. .792

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5240066"

/lab_host="DH10B"

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/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

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ORIGIN

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Query Match          39.7%; Score 739.8; DB 12; Length 792;
Best Local Similarity 98.7%; Pred. No. 2.9e-206;
Matches 767; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

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Db      1 CTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGAAGAGCCG 60

Qy     1053 CGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCCTGAAGAA 1112
          |||
Db      61 CGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCCTGAAGAA 120

Qy     1113 ACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCGATGAGCC 1172
          |||
Db     121 ACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCGATGAGCC 180

Qy     1173 TGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGAGAACTG 1232
          |||
Db     181 TGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGAGAACTG 240

Qy     1233 TGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCATGTATGT 1292
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Db     241 TGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCATGTATGT 300

Qy     1293 GGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGG 1352
          |||
Db     301 GGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGG 360

Qy     1353 CACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGA 1412
          |||
Db     361 CACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGA 420

Qy     1413 CGACATTTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGA 1472
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Db     421 CGACATTTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGA 480

Qy     1473 GGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGCCTCGGGC 1532
          |||
Db     481 GGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGCCTCGGGC 540

Qy     1533 TGTCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATGCAGGCAT 1592
          |||
Db     541 TGTCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATGCAGGCAT 600

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Qy      1593 CTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGGAGGTCAA 1652
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Db      601 CTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGGAGGTCAA 660

Qy      1653 GGTTCCTGCGGACATCAGGTGCCCCGGG--TACAGTCATCGTCCCCTTTAGGACAGTAGAAG 1711
          |||
Db      661 GGTTCCTGCGGACATCAGGTGCACGGGGCTACAGTCATCGTCCCCTTTAGGACAGTAGAAG 720

Qy      1712 GGACAGCCAAGGGTGGCGGT--GAGGACTTTGAAGACACATATGGGGAGTTGGAATT 1766
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Db      721 GGACAGCCAAGGGTGGCGGTGACGGACTCTGAAGACACATATGGGGAGTTTGAAT 777

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RESULT 13

BX368185

LOCUS BX368185 920 bp mRNA linear EST 08-MAY-2003
 DEFINITION BX368185 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
 cDNA clone CS0DD006YJ07 5-PRIME, mRNA sequence.

ACCESSION BX368185

VERSION BX368185.1 GI:30445119

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 920)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 7256.r For
 more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0BAA006ZD07_CS00533_2&cluster=7256.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAA006ZD07_CS00533_2&cluster=7256.r).

Contact : Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Paraday Avenue Genoscope sequence ID : CS0BAA006ZD07_CS00533_2.

FEATURES

source

Location/Qualifiers

1. .920

/organism="Homo sapiens"

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/clone="CS0DD006YJ07"

/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 39.6%; Score 737.8; DB 13; Length 920;

Best Local Similarity 95.1%; Pred. No. 1.3e-205;

Matches 827; Conservative 0; Mismatches 33; Indels 10; Gaps 6;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db     50 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 109

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Db    110 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 169

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG 180
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Db    230 CCAATCTGGTACCCGAGAACCCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 289

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Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
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Db    825 ATGCCCAAAAAGTCCCG-ACAGACCAACCCGNGGGATTT----TCTAGAGACCGAGGTGC 879
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Qy 841 CACCCTAAGGGCATTGAGATGGATGGGAAA 870
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RESULT 14
 AK035163

LOCUS AK035163 4374 bp mRNA linear HTC 18-SEP-2003
 DEFINITION Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430095C22 product:SODIUM/CALCIUM EXCHANGER 2 PRECURSOR (NA+)/CA(2+)-EXCHANGE PROTEIN 2) homolog [Rattus norvegicus], full insert sequence.

ACCESSION AK035163
 VERSION AK035163.1 GI:26084435
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
 AUTHORS Carninci,P. and Hayashizaki,Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE 2
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE 3
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4374)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cdNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .4374
 /organism="Mus musculus"
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 /strain="C57BL/6J"
 /db_xref="FANTOM_DB:9430095C22"
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 /note="SODIUM/CALCIUM EXCHANGER 2 PRECURSOR (NA(+)/CA(2+)-EXCHANGE PROTEIN 2) homolog [Rattus norvegicus] (SWISSPROT|P48768, evidence: FASTY, 97%ID, 100%length, match=2763) putative"

ORIGIN

Query Match 38.1%; Score 710.4; DB 11; Length 4374;
 Best Local Similarity 65.9%; Pred. No. 4.5e-197;
 Matches 1092; Conservative 0; Mismatches 536; Indels 30; Gaps 3;

Qy 136 GAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTGCCAATCTGGTACCCG 195
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Db	401	GAAGGCTGCCAAGGTTCTTACCGCTGCCAACCAGGTGTGCTGCTGCCTGTGTGGGAACCC	460
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Db	461	GAGGACCCATCGCTGGGCGACAAGGTTGCACGGGCCGTGGTGTACTTTGTGGCCATGGTC	520
Qy	256	TACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATC	315
Db	521	TACATGTTCTTGGGTGTGTCTATCATTGCCGATCGATTTATGGCATCCATTGAGGTCATC	580
Qy	316	ACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACT	375
Db	581	ACATCCAAGGAGAAAGAGATCACCATCACCAGGCAAATGGGGAGACCAGCGTGGGCACG	640
Qy	376	ATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCTTATGGCCCTGGGTTCTCTGCT	435
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Qy	436	CCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCAATTGCTGGTGATCTG	495
Db	701	CCTGAGATTCTGTTGACTGTCATCGAGGTCTGTGGCCACAACCTCCAGGCCGGTGAGCTA	760
Qy	496	GGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGT	555
Db	761	GGCCAGGCACCATCGTGGGCAGTGCCGCCTTCAACATGTTTGTGGTCATTGCTGTTTGT	820
Qy	556	GTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATC	615
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 Db 1361 ATGACAGGTGCGGGCAATGTGCTGCGCAGACATGCTGCGGATGCTGCCCGCAGG---CCG 1417

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 Db 1418 GGAGCCACCGATGGTGCCCCCGATGATGAGGACGATGGTGCCAGTCGCATCTTCTTTGAG 1477

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 Db 1478 CCCAGCCTCTATCACTGCCTGGAAAACTGCGGGTCAGTGCTGCTGTCCGTGGCTTGCCAG 1537

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Qy 1324 GCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAG 1383
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Qy 1444 GTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCA 1503
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 Db 1766 ---CCCGACGGCGGTGGGCGGCCCAAGGGGCGGCTGGTGGCGCCGCTGCTGGCCACTGTC 1822

Qy 1564 ACCATCTTGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTC 1623
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 Db 1823 ACCATCCTGGACGACGACCACGCGGGCATCTTCTCCTTCCAGGACCGCCTGCTGCATGTG 1882

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Qy 1684 GTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAA 1743
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Qy 1744 GACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC 1781
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RESULT 15

BX390204

LOCUS

BX390204

922 bp

mRNA

linear

EST 08-MAY-2003

DEFINITION BX390204 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
cDNA clone CS0DD006YJ07 5-PRIME, mRNA sequence.

ACCESSION BX390204

VERSION BX390204.1 GI:30461412

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 922)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7256.r For
more information about this cluster, see
[http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAG010ZA11_CS00945_1&cluster=7256.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAG010ZA11_CS00945_1&cluster=7256.r).
Contact : Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAG010ZA11_CS00945_1.

FEATURES

source Location/Qualifiers

1. .922

/organism="Homo sapiens"

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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 38.0%; Score 708.4; DB 13; Length 922;
Best Local Similarity 91.9%; Pred. No. 6e-197;
Matches 847; Conservative 0; Mismatches 66; Indels 9; Gaps 9;

Qy 30 CTCTGCCTTCCTCCATTTTGGGCTGGTTACCTTTGTGCTCTTCCTGAATGGTCTTCGAGC 89
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Db 3 CTCTGCCTTCCTCC-TTTTGGGCTGGTTACCTTTGTGCTCTTCCTG-ATGGTCTTCGAGC 60

Qy 90 AGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAAATGAGTCCTGTTTCAGG 149
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Db 61 AGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAAATGAGTCCTGTTTCAGG 120

Qy 150 GTCATCGGACTGCAAGGAGGGTGTCACTCTGCCAATCTGGTACCCGGAGAACCCTTCCCT 209
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Db 121 GTCATCGGACTGCAAGGAGGGTGTCACTCTGCCAATCTGGTACCCGGAGAACCCTTCCCT 180

Qy 210 TGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTTCCTTGG 269
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 04:06:20 ; Search time 7009.69 Seconds
(without alignments)
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Perfect score: 1863
Sequence: 1 atggcgtgggtaaggttgca.....ggaaagccagtattgggtga 1863

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1784.6	95.8	3812	6	AX496815		AX496815 Sequence
5	1784.4	95.8	2534	9	HSNCX22		X93017 Homo sapien
6	1783	95.7	2781	6	AX299471		AX299471 Sequence
7	1783	95.7	2782	6	AX476818		AX476818 Sequence
8	1783	95.7	2837	9	HSA304853		AJ304853 Homo sapi
9	1783	95.7	2966	6	AX480881		AX480881 Sequence
10	1783	95.7	5250	9	AF510501		AF510501 Homo sapi
11	1783	95.7	5268	9	AF510502		AF510502 Homo sapi
12	1782.8	95.7	126512	6	AX476820		AX476820 Sequence
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c 18	1544.4	82.9	183707	10	AC124384		AC124384 Mus muscu
19	1544	82.9	1784	10	AF321404		AF321404 Mus muscu
20	1544	82.9	3435	10	AF453257		AF453257 Mus muscu
21	1527	82.0	4854	10	RNU53420		U53420 Rattus norv
22	1526.8	82.0	247722	2	AC099080		AC099080 Rattus no
23	1331.4	71.5	3838	9	HSA508602		AJ508602 Homo sapi
24	938.6	50.4	77568	2	AC139418		AC139418 Homo sapi
c 25	913.2	49.0	77568	2	AC139418		AC139418 Homo sapi
26	810.6	43.5	4087	4	BOVEXCHANG		L06438 Bos taurus
27	810.6	43.5	4087	6	AX360315		AX360315 Sequence
28	805.2	43.2	3199	4	DOGSNCE		M57523 Dog cardiac
29	799.4	42.9	3150	4	CATSCE		L35846 Felis catus
30	796.2	42.7	3292	4	OCU52665		U52665 Oryctolagus
31	795	42.7	1920	4	FCNCX1S4		U67075 Felis catus
32	792.8	42.6	1832	9	AF109888		AF109888 Macaca mu
33	792.8	42.6	2965	9	AF107593		AF107593 Macaca mu

34	786.4	42.2	3184	9	HUMNACAA	M96368 Homo sapien
35	785.2	42.1	2129	9	HSNCX12	X91213 H.sapiens n
36	785.2	42.1	179343	9	AC007281	AC007281 Homo sapi
37	784.8	42.1	2814	9	AF108389	AF108389 Homo sapi
38	784.8	42.1	2883	9	AF108388	AF108388 Homo sapi
39	784.8	42.1	3002	9	AF128524	AF128524 Homo sapi
40	784.8	42.1	3250	9	HUMCNC	M91368 Human Na+/C
41	784.4	42.1	6023	9	HSM808447	BX648299 Homo sapi
42	783.4	42.1	3168	10	CPU04955	U04955 Cavia porce
43	765.8	41.1	2805	10	AF109163	AF109163 Rattus no
44	765.8	41.1	3037	10	RNSCEA1	X68812 R.norvegicu
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ALIGNMENTS

RESULT 1

AX496813

LOCUS AX496813 1863 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 3 from Patent WO02059316.

ACCESSION AX496813

VERSION AX496813.1 GI:23342336

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Hilbun,E. and Friddle,C.J.

TITLE Human ion exchanger proteins and polynucleotides encoding the same

JOURNAL Patent: WO 02059316-A 3 01-AUG-2002;

LEXICON GENETICS INC (US)

FEATURES Location/Qualifiers

source 1. .1863
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1863; DB 6; Length 1863;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1863; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG	180
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Db	181	 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
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Db	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
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Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
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Db	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	1800
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG	1860
Db	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG	1860
Qy	1861	TGA	1863
Db	1861	TGA	1863

RESULT 2

AF510503

LOCUS AF510503 5146 bp mRNA linear PRI 30-OCT-2002

DEFINITION Homo sapiens Na⁺/Ca²⁺ exchanger isoform 3 splice variant 4 (SLC8A3)
mRNA, complete cds; alternatively spliced.

ACCESSION AF510503

VERSION AF510503.1 GI:24421224

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 5146)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE The human SLC8A3 gene and the tissue-specific Na⁽⁺⁾/Ca⁽²⁺⁾
exchanger 3 isoforms

JOURNAL Gene 298 (1), 1-7 (2002)

MEDLINE 22294016

PUBMED 12406570

REFERENCE 2 (bases 1 to 5146)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE Direct Submission

JOURNAL Submitted (09-MAY-2002) Department of Biology, Univ. of Padova, via
G. Colombo, Padova, PD 35131, Italy

FEATURES Location/Qualifiers

source

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/mol_type="mRNA"

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/chromosome="14"

/map="14q24.2"

gene

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/gene="SLC8A3"

5'UTR

1. .754

/gene="SLC8A3"

CDS

755. .2617

/gene="SLC8A3"

/note="NCX3.4; expressed in skeletal muscle; alternatively
spliced"

/codon_start=1

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/db_xref="GI:24421225"

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3'UTR

2618. .5146

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5117. .5122
/gene="SLC8A3"

ORIGIN

Query Match 99.9%; Score 1861.4; DB 9; Length 5146;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1862; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db    815 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 874

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTCAAGGTCATCGGACTGCAAGGAGGGTGTATCCTG 180
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Db    875 ACAGGGCAGAACAATGAGTCCTGTTCAAGGTCATCGGACTGCAAGGAGGGTGTATCCTG 934

Qy    181 CCAATCTGGTACCCGAGAACCCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db    935 CCAATCTGGTACCCGAGAACCCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 994

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Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1655	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1714
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Db	1715	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1774
Qy	1021	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
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Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
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Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
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Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	2135	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2194
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	2195	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2254
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	2255	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	2314
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RESULT 3

AX496811

LOCUS AX496811 2766 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 1 from Patent WO02059316.

ACCESSION AX496811

VERSION AX496811.1 GI:23342335

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Hilbun,E. and Friddle,C.J.

TITLE Human ion exchanger proteins and polynucleotides encoding the same

JOURNAL Patent: WO 02059316-A 1 01-AUG-2002;

LEXICON GENETICS INC (US)

FEATURES Location/Qualifiers

source 1..2766
/organism="Homo sapiens"
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ORIGIN

Query Match 95.8%; Score 1784.6; DB 6; Length 2766;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

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Db	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
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Qy	361	ACCAGCACAAACCACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
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Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960

Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
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Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC---TGTGAAAACCATAAG	1796

Qy 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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RESULT 4

AX496815

LOCUS AX496815 3812 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 5 from Patent WO02059316.

ACCESSION AX496815

VERSION AX496815.1 GI:23342337

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Hilbun,E. and Friddle,C.J.

TITLE Human ion exchanger proteins and polynucleotides encoding the same

JOURNAL Patent: WO 02059316-A 5 01-AUG-2002;

LEXICON GENETICS INC (US)

FEATURES

source Location/Qualifiers
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ORIGIN

Query Match 95.8%; Score 1784.6; DB 6; Length 3812;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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 Db 618 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 677
 Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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 Db 678 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 737
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 Db 738 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG 797
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 Db 798 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 857
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 Qy 301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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 Db 918 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 977
 Qy 361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

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Db	1038	 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	1097
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1098	 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1157
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	1158	 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	1217
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Db	1218	 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1277
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1278	 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1337
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1338	 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1397
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1398	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1457
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1458	 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1517
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1518	 CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1577
Qy	961	AAGGATCTGAAGCAAAAAACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1578	 AAGGATCTGAAGCAAAAAACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1637
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Db	1638	 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1697
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1698	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1757
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1758	 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1817
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Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db 1998 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 2057

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Db 2058 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 2117

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Db 2118 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 2177

Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db 2178 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 2237

Qy 1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
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Db 2238 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 2297

Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db 2298 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2357

Qy 1741 GAAGACACATATGGGGAGTTGGAATCAAGAATGATGAACTGTATGTGACAGACAGGAA 1800
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Db 2358 GAAGACACATATGGGGAGTTGGAATCAAGAATGATGAAAC----TGTGAAAACCATAAG 2413

Qy 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db 2414 GGTATAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2454

RESULT 5

HSNCX22

LOCUS HSNCX22 2534 bp DNA linear PRI 12-NOV-2000

DEFINITION Homo sapiens partial SCL8A3 gene for solute carrier family 8 (sodium/calcium exchanger), member 3 (SCL8A3), exon 2.

ACCESSION X93017

VERSION X93017.1 GI:1067133

KEYWORDS SLC8A3 gene; sodium-calcium exchanger.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Kraev,A., Chumakov,I. and Carafoli,E.

TITLE The organization of the human gene NCX1 encoding the sodium-calcium exchanger
 JOURNAL Genomics 37 (1), 105-112 (1996)
 MEDLINE 97079665
 PUBMED 8921376
 REFERENCE 2 (bases 1 to 2534)
 AUTHORS Kraev,A.S.
 TITLE Direct Submission
 JOURNAL Submitted (14-NOV-1995) A.S. Kraev, Swiss Federal Institute of Technology, Laboratory of Biochemistry III, Universitaetstr. 16, Zurich, CH-8092, SWITZERLAND
 COMMENT Similar to X91213.
 FEATURES Location/Qualifiers
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 gene 281..2126
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 /number=2

ORIGIN

Query Match 95.8%; Score 1784.4; DB 9; Length 2534;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      61 TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db      403 TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy      121 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTCCTG 180
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Qy      181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Qy      241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db      583 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642

Qy      301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

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Db	643	 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	702
Qy	361	ACCAGCACAACCACTATTCTGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	703	 ACCAGCACAACCACTATTCTGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	762
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
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Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
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Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	883	 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	942
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	943	 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1002
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1003	 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1062
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1063	 TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1122
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1123	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1182
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATCCCATTTTCTAGATGGGAAC	900
Db	1183	 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATCCCATTTTCTAGATGGGAAC	1242
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1243	 CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1302
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Db	1303	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1362
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Db	1363	 TACTATGCTCTTTCCCAACAGAAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1422
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Db	1423	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1482
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Db	1483	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1542
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1543	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1602
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1603	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1662
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1663	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1722
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	1440
Db	1723	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	1782
Qy	1441	TTTGTAAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
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Db	1843	GCAATATTCAACAGTCTTCCCTTGCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1902
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1903	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1962
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1963	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	2022
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
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Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTAT	1786
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RESULT 6

AX299471

LOCUS	AX299471	2781 bp	DNA	linear	PAT 26-NOV-2001
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DEFINITION Sequence 1 from Patent WO0183744.

ACCESSION AX299471

VERSION AX299471.1 GI:17129228

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Wilm, C.

TITLE Sodium-calcium exchanger protein

JOURNAL Patent: WO 0183744-A 1 08-NOV-2001;
MERCK PATENT GmbH (DE)

FEATURES Location/Qualifiers

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ORIGIN

Query Match 95.7%; Score 1783; DB 6; Length 2781;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
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Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
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Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
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RESULT 7

AX476818

LOCUS AX476818 2782 bp DNA linear PAT 12-AUG-2002

DEFINITION Sequence 1 from Patent WO0233086.

ACCESSION AX476818

VERSION AX476818.1 GI:22216098

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Merkulov,G.V., Ketchum,K.A., Shao,W., Yan,C., di Francesco,V. and Beasley,E.M.

TITLE Isolated human transporter proteins, nucleic acid molecules encoding human transporter proteins, and uses thereof

JOURNAL Patent: WO 0233086-A 1 25-APR-2002;
PE Corporation (NY) (US)

FEATURES Location/Qualifiers

source 1. .2782

/organism="Homo sapiens"

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ORIGIN

Query Match 95.7%; Score 1783; DB 6; Length 2782;

Best Local Similarity 98.4%; Pred. No. 0;

Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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RESULT 8

HSA304853

LOCUS HSA304853 2837 bp mRNA linear PRI 06-JUN-2001

DEFINITION Homo sapiens mRNA for sodium/calcium exchanger, SCL8A3, alternative splice form B (SCL8A3 gene).

ACCESSION AJ304853

VERSION AJ304853.1 GI:14330384

KEYWORDS alternative splicing; form B; SCL8A3 gene; SCL8A3 protein; Sodium/calcium exchanger.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Gabellini,N.

TITLE Characterization of the human SCL8A3 gene for solute carrier family 8, member 3 (sodium/calcium exchanger)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2837)

AUTHORS Bortoluzzi,S.

TITLE Direct Submission

JOURNAL Submitted (22-DEC-2000) Bortoluzzi S., Department of Biology and Department of Biological Chemistry, University of Padova, via G. Colombo 3, 35131 PADOVA, ITALY

FEATURES Location/Qualifiers

source 1..2837

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      /note="alternative splice form B (exons 2, 4, 5, 9, 10,
11, 12)"
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ORIGIN

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Query Match          95.7%;  Score 1783;  DB 9;  Length 2837;
Best Local Similarity 98.4%;  Pred. No. 0;
Matches 1812;  Conservative 0;  Mismatches 25;  Indels 4;  Gaps 1;

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Db 1623 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1682

Qy 1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db 1683 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1742

Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db 1743 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1802

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA 1800
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Db 1803 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1858

Qy 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db 1859 GGT'AAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1899

RESULT 9

AX480881

LOCUS AX480881 2966 bp DNA linear PAT 12-AUG-2002

DEFINITION Sequence 41 from Patent WO0246415.

ACCESSION AX480881

VERSION AX480881.1 GI:22217538


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KEYWORDS      .
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
AUTHORS       Lee,E.A., Baughn,M.R., Yue,H., Ding,L., Raumann,B.E., Hafalia,A.J.,
              Khan,F.A., Nguyen,D.B., Elliott,V.S., Ramkumar,J., Walia,N.K.,
              Ison,C.H., Lu,Y., Gandhi,A.R., Warren,B.A., Duggan,B.M.,
              Tribouley,C.M., Burford,N., Lu,D.A., Lal,P.G., Yao,M.G., Xu,Y.,
              Bruns,C.M., Thangavelu,K., Swarnakar,A., Tang,Y.T., Azimzai,Y.,
              Thornton,M., Arvizu,C. and Policky,J.L.
TITLE         Transporters and ion channels
JOURNAL       Patent: WO 0246415-A 41 13-JUN-2002;
              Incyte Genomics, Inc. (US)
FEATURES      Location/Qualifiers
source        1. .2966
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               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
               /note="Incyte ID No: 5923789CB1"
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Qy	61	TTTGTGCTCTTCTCGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	261	TTTGTGCTCTTCTCGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	320
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Db	321	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	380
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	381	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	440
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	441	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	500
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCAATGGAGAA	360
Db	501	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCAATGGAGAA	560
Qy	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	561	ACCAGCACAACTACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	620
Qy	421	CTGGGTTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480

Db	621	CTGGGTTCTCTGCTCCTGAGATACTCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCT	680
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	681	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	740
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Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	801	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	860
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	861	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	920
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	921	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	980
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	981	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1040
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1041	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1100
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1101	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1160
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Db	1161	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1220
Qy	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1221	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1280
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1281	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1340
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1341	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1400
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1401	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1460
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1461	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1520

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 Db 1521 AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1580
 Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
 |||
 Db 1581 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1640
 Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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 Db 1641 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1700
 Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
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 Db 1701 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1760
 Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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 Db 1761 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1820
 Qy 1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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 Db 1821 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1880
 Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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 Db 1881 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1940
 Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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 Db 1941 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAAC----TGTGAAAACCATAAG 1996
 Qy 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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 Db 1997 GGTAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2037

RESULT 10

AF510501

LOCUS AF510501 5250 bp mRNA linear PRI 30-OCT-2002

DEFINITION Homo sapiens Na⁺/Ca²⁺ exchanger isoform 3 splice variant 2 (SLC8A3) mRNA, complete cds; alternatively spliced.

ACCESSION AF510501

VERSION AF510501.1 GI:24421220

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 5250)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE The human SLC8A3 gene and the tissue-specific Na⁽⁺⁾/Ca⁽²⁺⁾ exchanger 3 isoforms

JOURNAL Gene 298 (1), 1-7 (2002)

MEDLINE 22294016

PUBMED 12406570

Db	815	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	874
Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	875	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	934
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	935	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	994
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	995	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	1054
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAAATTAAGAAACCCAATGGAGAA	360
Db	1055	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAAATTAAGAAACCCAATGGAGAA	1114
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	1115	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	1174
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
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Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
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Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
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Db	1355	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1414
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1415	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1474
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1475	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1534
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1535	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1594
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1595	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1654
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1655	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1714

Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
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Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1775	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1834
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1835	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1894
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1895	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1954
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1955	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	2014
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	2015	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	2074
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Db	2255	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	2314
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Db	2315	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	2374
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	2375	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	2434
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	2435	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	2494
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	1800
Db	2495	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG	2550

Qy 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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 Db 2551 GGT TAA AATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2591

RESULT 11

AF510502

LOCUS AF510502 5268 bp mRNA linear PRI 30-OCT-2002

DEFINITION Homo sapiens Na⁺/Ca²⁺ exchanger isoform 3 splice variant 3 (SLC8A3) mRNA, complete cds; alternatively spliced.

ACCESSION AF510502

VERSION AF510502.1 GI:24421222

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 5268)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE The human SLC8A3 gene and the tissue-specific Na⁽⁺⁾/Ca⁽²⁺⁾ exchanger 3 isoforms

JOURNAL Gene 298 (1), 1-7 (2002)

MEDLINE 22294016

PUBMED 12406570

REFERENCE 2 (bases 1 to 5268)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE Direct Submission

JOURNAL Submitted (09-MAY-2002) Department of Biology, Univ. of Padova, via G. Colombo, Padova, PD 35131, Italy

FEATURES Location/Qualifiers

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gene

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5'UTR

1. .754
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CDS

755. .3538
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 /note="NCX3.3; expressed in skeletal muscle; alternatively spliced"
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 DFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTE
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ORIGIN

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Query Match 95.7%; Score 1783; DB 9; Length 5268;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	815	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	874
Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	875	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	934
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	935	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	994
Qy	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	995	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	1054
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	1055	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	1114
Qy	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	1115	ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	1174
Qy	421	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	1175	CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	1234
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1235	ATTGCTGGTGATCTGGGACCTTCTACCATTTAGGGAGTGCAGCCTTCAACATGTTTCATC	1294
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	1295	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	1354

Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	1355	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1414
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1415	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1474
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1475	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1534
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1535	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1594
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1595	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1654
Qy	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1655	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1714
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1715	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1774
Qy	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1775	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1834
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1835	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1894
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1895	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1954
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1955	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	2014
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	2015	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	2074
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	2075	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	2134
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	2135	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2194

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Qy      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db      2195 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 2254

Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db      2255 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 2314

Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db      2315 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 2374

Qy      1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db      2375 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2434

Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db      2435 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2494

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Db      2495 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2550

Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db      2551 GGTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2591

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RESULT 12

AX476820

LOCUS AX476820 126512 bp DNA linear PAT 12-AUG-2002

DEFINITION Sequence 3 from Patent WO0233086.

ACCESSION AX476820

VERSION AX476820.1 GI:22216099

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Merkulov,G.V., Ketchum,K.A., Shao,W., Yan,C., di Francesco,V. and
Beasley,E.M.

TITLE Isolated human transporter proteins, nucleic acid molecules
encoding human transporter proteins, and uses thereof

JOURNAL Patent: WO 0233086-A 3 25-APR-2002;
PE Corporation (NY) (US)

FEATURES Location/Qualifiers

source 1. .126512
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 95.7%; Score 1782.8; DB 6; Length 126512;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db	2010	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	2069
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	2070	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	2129
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG	180
Db	2130	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG	2189
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	2190	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	2249
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTTGCTGACCGCTTCATGGCA	300
Db	2250	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATTTGCTGACCGCTTCATGGCA	2309
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	2310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	2369
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	2370	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	2429
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	2430	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	2489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	2490	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	2549
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	2550	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	2609
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	2610	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	2669
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	2670	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	2729
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	2730	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	2789
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Db	2790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	2849

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Qy	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	2910	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	2969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	2970	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	3029
Qy	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
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Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1140
Db	3090	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	3149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
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Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	3210	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	3269
Qy	1261	AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	3270	AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	3329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	3330	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	3389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Db	3390	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	3449
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	3450	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	3509
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCCTAGCCTCCCCCTTGTGTGGCCACA	1560
Db	3510	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCCTAGCCTCCCCCTTGTGTGGCCACA	3569
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	3570	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	3629
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	3630	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	3689
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Db      3750 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGTGT 3795

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RESULT 13

AF508982

LOCUS AF508982 145118 bp DNA linear PRI 24-OCT-2002

DEFINITION Homo sapiens Na⁺/Ca²⁺ exchanger isoform 3 (SLC8A3) gene, promoter region and complete cds.

ACCESSION AF508982

VERSION AF508982.1 GI:22087482

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 145118)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE The human SLC8A3 gene and the tissue-specific Na⁺/Ca²⁺ exchanger 3 isoforms

JOURNAL Gene 298 (1), 1-7 (2002)

REFERENCE 2 (bases 1 to 145118)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE Control of the Na⁺/Ca²⁺ exchanger 3 promoter by cAMP and Ca²⁺ in differentiating neurons

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 145118)

AUTHORS Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.

TITLE Direct Submission

JOURNAL Submitted (02-MAY-2002) Department of Biology, University of Padova, via G. Colombo 3, Padova, PD 35131, Italy

FEATURES Location/Qualifiers

source 1. .145118
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/db_xref="taxon:9606"
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/gene="SLC8A3"

promoter 1. .263
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TATA_signal 236. .241
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polyA_signal 145089. .145094
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db 20915 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 20974
Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db 20975 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 21034
Qy 121 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGGTGTCATCCTG 180
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Db 21035 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGGTGTCATCCTG 21094
Qy 181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db 21095 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 21154
Qy 241 TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 300
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Db 21155 TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 21214
Qy 301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

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Db	21215	 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	21274
Qy	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	21275	 ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	21334
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	21335	 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	21394
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	21395	 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	21454
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	21455	 ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	21514
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	21515	 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	21574
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	21575	 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	21634
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	21635	 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	21694
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	21695	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	21754
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	21755	 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	21814
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Db	21815	 CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	21874
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Db	21875	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	21934
Qy	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	21935	 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	21994
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	21995	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	22054
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Db 22055 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 22114

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Db 22115 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 22174

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Qy 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db 22235 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 22294

Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db 22295 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 22354

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Db 22415 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 22474

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Db 22475 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 22534

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Db 22535 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 22594

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Db 22595 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 22654

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Db 22655 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 22700

RESULT 14

AC009607

LOCUS AC009607 146055 bp DNA linear HTG 04-MAY-2001

DEFINITION Homo sapiens clone RP11-1I11, WORKING DRAFT SEQUENCE, 31 unordered pieces.

ACCESSION AC009607

VERSION AC009607.3 GI:8072446

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 146055)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens, clone RP11-1I11
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 146055)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
 Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
 Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
 Cooke,P., DeArellano,K., Depayre,E., Devon,K., Dewar,K.,
 Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,
 Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
 Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
 Karatas,A., Lehoczký,J., Lieu,C., Locke,K., Macdonald,P.,
 Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,
 Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,
 Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
 Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
 Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
 Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
 Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.

TITLE Direct Submission
 JOURNAL Submitted (28-AUG-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT On May 25, 2000 this sequence version replaced gi:7321520.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L1464

Center clone name: 1_I_11

----- Summary Statistics

Sequencing vector: M13; M77815; 99% of reads

Sequencing vector: Plasmid; n/a; %-0.f%% of reads

0.776287932251235Chemistry: Dye-primer-amersham; 6% of reads

Chemistry: Dye-terminator Big Dye; 94% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 126247 bases at least Q40

Consensus quality: 134710 bases at least Q30

Consensus quality: 138332 bases at least Q20

Insert size: 160000; agarose-fp

Insert size: 143055; sum-of-contigs

Quality coverag.

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 31 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1166: contig of 1166 bp in length
 * 1167 1266: gap of 100 bp
 * 1267 2417: contig of 1151 bp in length
 * 2418 2517: gap of 100 bp

*	2518	3635: contig of 1118 bp in length
*	3636	3735: gap of 100 bp
*	3736	4851: contig of 1116 bp in length
*	4852	4951: gap of 100 bp
*	4952	6701: contig of 1750 bp in length
*	6702	6801: gap of 100 bp
*	6802	8629: contig of 1828 bp in length
*	8630	8729: gap of 100 bp
*	8730	10482: contig of 1753 bp in length
*	10483	10582: gap of 100 bp
*	10583	12126: contig of 1544 bp in length
*	12127	12226: gap of 100 bp
*	12227	13831: contig of 1605 bp in length
*	13832	13931: gap of 100 bp
*	13932	16132: contig of 2201 bp in length
*	16133	16232: gap of 100 bp
*	16233	17951: contig of 1719 bp in length
*	17952	18051: gap of 100 bp
*	18052	20069: contig of 2018 bp in length
*	20070	20169: gap of 100 bp
*	20170	22565: contig of 2396 bp in length
*	22566	22665: gap of 100 bp
*	22666	24924: contig of 2259 bp in length
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*	26997	27096: gap of 100 bp
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*	112313	112412: gap of 100 bp
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misc_feature	22666. .24924 /note="assembly_fragment"
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ORIGIN

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Best Local Similarity 99.9%;  Pred. No. 0;
Matches 1784;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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138634

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138814

Qy          241 TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 300
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Db 140015 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 140074

Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db 140075 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 140134

Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy 1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db 140255 ACAGTCATCGTCCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 140314

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Db 140315 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTGT 140360

RESULT 15
CNS01RGT
LOCUS CNS01RGT 206256 bp DNA linear PRI 10-JUL-2001
DEFINITION Human chromosome 14 DNA sequence BAC R-486013 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION AL160191
VERSION AL160191.3 GI:14715172
KEYWORDS HTG; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 206256)
AUTHORS Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
Gyapay,G., Saurin,W. and Weissenbach,J.
TITLE Sequencing of the human chromosome 14
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 206256)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT On Jul 12, 2001 this sequence version replaced gi:7708226.
----- Genome Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: <http://www.genoscope.cns.fr/>
Contact: SeqRef@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-718G2 (AC=AL356804)
Downstream BAC (overlapping the SP6 end) : R-1023I22
----- Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 8.36x in Q20 bases; sum-of-contigs

Overall quality chart :
Range : bases
0 :
1 - 9 : 7
10 - 19 : 78
20 - 29 : 197
30 - 39 : 1106
40 - 49 : 5627
50 - 59 : 11755
60 - 69 : 10922
70 - 79 : 18529
80 - 89 : 46808
90 - 99 : 111227

Percentage of bases with a quality value >= 40 : 99 %.
FEATURES Location/Qualifiers

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ORIGIN

Query Match 95.7%; Score 1782.8; DB 9; Length 206256;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy    121 ACAGGGCAGAACAAATGAGTCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180
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Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Qy    361 ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy    421 CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 480
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Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	900
Db	96235	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	96294
Qy	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	96295	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	96354
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	96355	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	96414
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
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Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
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Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	96535	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	96594
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	96595	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	96654
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	96655	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	96714
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	96715	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	96774
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	96775	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	96834
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	96835	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	96894
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	96895	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	96954
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	96955	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	97014
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680

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Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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Job time : 7017.69 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 00:42:04 ; Search time 653.599 Seconds
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Perfect score: 1863
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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			%	DB	Query	
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2	1784.6	95.8	2766	6	ABQ78861	Abq78861 Human ion
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4	1784.6	95.8	2769	6	ABQ78866	Abq78866 Human ion
5	1784.6	95.8	2769	6	ABQ78865	Abq78865 Human ion
6	1784.6	95.8	3812	6	ABQ78863	Abq78863 Human ion
7	1784.4	95.8	2534	7	ACC00414	Acc00414 Human 690

8	1783	95.7	2781	6	ABA04756	Aba04756	Human nat
9	1783	95.7	2782	6	ABN83428	Abn83428	Human tra
10	1783	95.7	2966	6	ABZ33735	Abz33735	Human TRI
11	1782.8	95.7	126512	6	ABN83429	Abn83429	Human tra
12	1782.4	95.7	2813	7	ABX56261	Abx56261	Human NOV
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16	785.2	42.1	1836	4	AAI19464	Aai19464	Probe #93
17	785.2	42.1	1836	4	ABA64480	Aba64480	Human foe
18	785.2	42.1	1836	4	AAI44657	Aai44657	Probe #13
19	785.2	42.1	1836	4	ABA31619	Aba31619	Probe #10
20	785.2	42.1	1836	4	AAK12937	Aak12937	Human bra
21	785.2	42.1	1836	4	ABS38231	Abs38231	Human liv
22	785.2	42.1	1836	6	ABS12734	Abs12734	Human gen
23	784.8	42.1	2814	4	AAH57377	Aah57377	Human hea
24	784.8	42.1	5438	5	ABV24305	Abv24305	Human pro
25	765.8	41.1	3037	9	ADB59225	Adb59225	Toxicity-
26	692.4	37.2	4282	8	AAL55587	Aal55587	Human 465
27	692.4	37.2	4291	3	AAC75706	Aac75706	Human ORF
28	319	17.1	4546	4	ABL09809	Abl09809	Drosophil
29	319	17.1	24221	4	ABL09808	Abl09808	Drosophil
30	164.2	8.8	459	4	AAI10174	Aai10174	Probe #10
31	164.2	8.8	459	4	ABA51807	Aba51807	Human foe
32	164.2	8.8	459	4	AAI31424	Aai31424	Probe #11
33	164.2	8.8	459	4	ABA21636	Aba21636	Probe #10
34	164.2	8.8	459	4	AAK00114	Aak00114	Human bra
35	164.2	8.8	459	4	ABS25121	Abs25121	Human liv
36	164.2	8.8	459	6	ABS00120	Abs00120	Human gen
37	79	4.2	477	8	ACH14793	Ach14793	Human adu
38	79	4.2	1187	5	AAS90968	Aas90968	DNA encod
39	79	4.2	1187	7	ACD05939	Acd05939	Novel hum
40	71.6	3.8	1617	6	ABZ14786	Abz14786	Arabidops
41	71.6	3.8	1617	7	ADA67812	Ada67812	Arabidops
42	71.6	3.8	1950	3	AAZ47475	Aaz47475	Arabidops
c 43	68.2	3.7	303	4	AAH57169	Aah57169	Human hea
44	57.2	3.1	2000	7	ADA71938	Ada71938	Rice gene
45	44.8	2.4	2803	3	AAZ47476	Aaz47476	11 transm

ALIGNMENTS

RESULT 1

ABQ78862

ID ABQ78862 standard; cDNA; 1863 BP.

XX

AC ABQ78862;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #2 cDNA.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;

KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;

KW gene; ss; chromosome 14.

XX

OS Homo sapiens.
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 FH Key Location/Qualifiers
 FT CDS 1..1863
 FT /*tag= a
 FT /product= "Ion exchanger protein 2"
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 PN WO200259316-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 22-JAN-2002; 2002WO-US001817.
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 PR 23-JAN-2001; 2001US-0263384P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Friddle CJ, Hilbun E;
 XX
 DR WPI; 2002-599791/64.
 DR P-PSDB; ABB81914.
 XX
 PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.
 XX
 PS Disclosure; Page 39-40; 42pp; English.
 XX
 CC The invention relates to a novel human ion exchanger protein (NHIEP),
 CC that shares structural similarity with mammalian sodium-calcium exchanger
 CC proteins, and potassium dependent versions of the same. The NHIEP of the
 CC invention has nootropic, cytostatic, antiarthritic, and virucide
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
 CC or to therapeutically augment the efficacy of chemotherapeutic agents
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The
 CC sequence encodes a NHIEP of the invention
 XX
 SQ Sequence 1863 BP; 464 A; 426 C; 514 G; 459 T; 0 U; 0 Other;

Query Match 100.0%; Score 1863; DB 6; Length 1863;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1863; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180

Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCTTGGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
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Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
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Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
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Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
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Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCTATTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCTATTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
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Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
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Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA	1800
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG	1860
Db	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG	1860
Qy	1861	TGA 1863 	

Db 1861 TGA 1863

RESULT 2

ABQ78861

ID ABQ78861 standard; cDNA; 2766 BP.

XX

AC ABQ78861;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;

KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;

KW gene; ss; chromosome 14.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .2766

FT /*tag= a

FT /product= "Ion exchanger protein 1"

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

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PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

DR P-PSDB; ABB81913.

XX

PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.

XX

PS Claim 1; Page 36-37; 42pp; English.

XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence encodes a NHIEP of the invention

XX

SQ Sequence 2766 BP; 655 A; 678 C; 760 G; 673 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 6; Length 2766;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

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Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCAATGGAGAA	360
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Qy	361	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	361	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCCTTATGGCC	420
Qy	421	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	421	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
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Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780

Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	900
Db	841	CACCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
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Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGATGAACACTTC	1440
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Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
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Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680

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      |||
Db      1621  GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
Qy      1681  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
      |||
Db      1681  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
Qy      1741  GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAACTGTATGTGACAGACAGGAA 1800
      |||
Db      1741  GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAAC----TGTGAAAACCATAAG 1796
Qy      1801  GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
      |||
Db      1797  GGTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837

```

RESULT 3

ABQ78864

ID ABQ78864 standard; cDNA; 2766 BP.

XX

AC ABQ78864;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA A/G mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;

KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;

KW gene; ss; mutant.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT mutation replace(1889,A)

FT /*tag= a

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

XX

PT Novel polynucleotides encoding human ion exchanger proteins that are

PT structurally related to mammalian sodium-calcium exchanger proteins,

PT useful for drug screening, diagnosis and in gene therapy of biological

PT disorders.

XX

PS Disclosure; Page; 42pp; English.

Db	541	ATCATTTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440

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Qy      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
          |||
Db      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
          |||
Db      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620
          |||
Db      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620

Qy      1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
          |||
Db      1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680

Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
          |||
Db      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
          |||
Db      1741 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
          |||
Db      1797 GGTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837

```

RESULT 4

ABQ78866

ID ABQ78866 standard; cDNA; 2769 BP.

XX

AC ABQ78866;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA A/G+GCA mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
 KW gene; ss; mutant.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT mutation replace(1889,A)

FT /*tag= a

FT mutation replace(2113..2115,-)

FT /*tag= b

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.
 XX
 PR 23-JAN-2001; 2001US-0263384P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Friddle CJ, Hilbun E;
 XX
 DR WPI; 2002-599791/64.
 XX
 PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.
 XX
 PS Disclosure; Page; 42pp; English.
 XX
 CC The invention relates to a novel human ion exchanger protein (NHIEP),
 CC that shares structural similarity with mammalian sodium-calcium exchanger
 CC proteins, and potassium dependent versions of the same. The NHIEP of the
 CC invention has nootropic, cytostatic, antiarthritic, and virucide
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
 CC or to therapeutically augment the efficacy of chemotherapeutic agents
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The
 CC sequence represents a mutant form of a NHIEP of the invention. Note: The
 CC present sequence is not shown in the specification but is derived from
 CC the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)
 XX
 SQ Sequence 2769 BP; 655 A; 679 C; 762 G; 673 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 6; Length 2769;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTCAAGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	121	ACAGGGCAGAACAAATGAGTCCTGTTCAAGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360

Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCTATTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCTATTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200

Qy	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAACTGTATGTGACAGACAGGAA	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAAC----TGTGAAAACCATAAG	1796
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1841
Db	1797	GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA	1837

RESULT 5

ABQ78865

ID ABQ78865 standard; cDNA; 2769 BP.

XX

AC ABQ78865;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 cDNA GCA mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;

KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW gene; ss; mutant.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers
FT mutation replace(2113. .2115,-)

FT /*tag= a

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

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PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

XX

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PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.

XX

PS Disclosure; Page; 42pp; English.

XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a mutant form of a NHIEP of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)

XX

SQ Sequence 2769 BP; 656 A; 679 C; 761 G; 673 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 6; Length 2769;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
|||||

Db 1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
|||||

Db 61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTATGGCC	420
Db	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTATGGCC	420
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020

Db	961	AAGGATCTGAAGCAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG	1796
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1841

Db 1797 GGTAAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837

RESULT 6

ABQ78863

ID ABQ78863 standard; cDNA; 3812 BP.

XX

AC ABQ78863;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein cDNA #3.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;

KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;

KW gene; ss; chromosome 14.

XX

OS Homo sapiens.

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

XX

PT Novel polynucleotides encoding human ion exchanger proteins that are

PT structurally related to mammalian sodium-calcium exchanger proteins,

PT useful for drug screening, diagnosis and in gene therapy of biological

PT disorders.

XX

PS Disclosure; Page 41-42; 42pp; English.

XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),

CC that shares structural similarity with mammalian sodium-calcium exchanger

CC proteins, and potassium dependent versions of the same. The NHIEP of the

CC invention has nootropic, cytostatic, antiarthritic, and virucide

CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can

CC be targeted by drugs, oligos, antibodies etc., in order to treat disease

CC or to therapeutically augment the efficacy of chemotherapeutic agents

CC used in the treatment of cancer, arthritis, or as antiviral agents. The

CC sequence encodes a NHIEP of the invention, with regions of flanking

CC sequence

XX

SQ Sequence 3812 BP; 860 A; 1059 C; 1041 G; 852 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 6; Length 3812;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	618	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	677
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	678	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	737
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	738	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	797
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	798	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	857
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	858	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	917
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	918	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	977
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	978	ACCAGCACAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	1037
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	1038	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	1097
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1098	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1157
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	1158	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	1217
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	1218	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1277
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1278	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1337
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1338	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1397
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1398	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1457
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900

Db	1458	 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1517
Qy	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1518	 CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1577
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1578	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1637
Qy	1021	TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1638	 TACTATGCTCTTTCCCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1697
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1698	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1757
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1758	 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1817
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1818	 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1877
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1878	 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1937
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1938	 AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1997
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	1440
Db	1998	 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGTAGGAGGATGAACACTTC	2057
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	2058	 TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2117
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	2118	 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	2177
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTGAATGTGATACTATTCAT	1620
Db	2178	 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTGAATGTGATACTATTCAT	2237
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	2238	 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	2297
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740


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Db      2298 ACAGTCATCGTCCCTTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2357
QY      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
      |||
Db      2358 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2413
QY      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
      |||
Db      2414 GGTAAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2454

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ACC00414

XX

XX

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XX

KW Na⁺/Ca²⁺ exchanger; ion transporter; neural tissue;

KW neurological disorder; gene; ss.

XX

XX

FT	CDS	343.	.2130
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FT /*tag= a

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FT /product= "Human 69039"
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DR P-PSDB; ABR40134.

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XX

XX

CC cells as well as in neural tissues, e.g. brain cortex and hypothalamus.
CC 69039 may therefore be used for preparing a composition for treating
CC haematopoietic or neurological disorder

XX

SQ Sequence 2534 BP; 602 A; 595 C; 644 G; 693 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.4; DB 7; Length 2534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
      |||
Db    343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy      61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
      |||
Db    403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy     121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 180
      |||
Db    463 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 522

Qy     181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
      |||
Db    523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy     241 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 300
      |||
Db    583 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA 642

Qy     301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
      |||
Db    643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy     361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
      |||
Db    703 ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy     421 CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 480
      |||
Db    763 CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 822

Qy     481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
      |||
Db    823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 882

Qy     541 ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
      |||
Db    883 ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy     601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
      |||
Db    943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy     661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
      |||
Db   1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062
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Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1063	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1122
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1123	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1182
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1183	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1242
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1243	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1302
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1303	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1362
Qy	1021	TACTATGCTCTTTCCCAACAGAAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1363	TACTATGCTCTTTCCCAACAGAAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1422
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1140
Db	1423	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1482
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1483	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1542
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1543	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1602
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1603	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1662
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1663	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1722
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGATGAACACTTC	1440
Db	1723	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGATGAACACTTC	1782
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1783	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1842
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1843	GCAATATTCAACAGTCTTCCCTTGCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1902

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Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1903 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1962

Qy      1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1963 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 2022

Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
          ||||||||||||||||||||||||||||||||||||||||||||
Db      2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128

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RESULT 8

ABA04756

ID ABA04756 standard; cDNA; 2781 BP.

XX

AC ABA04756;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3, cDNA.

XX

KW Human; Natrium(+)-Calcium(2+) exchanger form 3; HNCX3; chromosome 14;
 KW cardiac failure; myocardial infarction; cardiac hypertrophy; arrhythmia;
 KW myocarditis; pulmonary hypertension; cardiotoxicity; cardiant; Vaccine;
 KW coronary heart disease; renal failure; ischaemic disorder;
 KW Antiarrhythmic; Vasotropic; Hypotensive; cardiovascular disorder; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .2781

FT /*tag= a

FT /partial

FT /product= "Human natrium(+)-calcium(2+) exchanger form 3
 FT protein, HNCX3"

FT /note= "No stop codon given"

XX

PN WO200183744-A2.

XX

PD 08-NOV-2001.

XX

PF 30-APR-2001; 2001WO-EP004886.

XX

PR 02-MAY-2000; 2000EP-00109080.

XX

PA (MERE) MERCK PATENT GMBH.

XX

PI Wilm C;

XX

DR WPI; 2002-041493/05.

DR P-PSDB; AAM47745.

XX
PT New polypeptide, useful as vaccines for inducing immune response against
PT diseases such as myocardial infarction, arrhythmia, ischemic disorders,
PT renal disorders in mammal.
XX
PS Claim 4; Page 34-38; 41pp; English.
XX
CC The present sequence is the coding sequence for human Sodium(+)-Calcium
CC (2+) exchanger form 3 (HNCX3). The HNCX3 gene maps to human chromosome
CC 14. HNCX3 and its coding sequence are useful for treating acute and
CC chronic cardiac failure of different aetiologies, myocardial infarction,
CC cardiac hypertrophy, arrhythmia, myocarditis, pulmonary hypertension,
CC cardiotoxicity (e.g. induced by chemotherapy), coronary heart disease,
CC acute and chronic renal failure, ischaemic disorders of skeletal muscle
CC and ischaemic brain disorders of different aetiologies
XX
SQ Sequence 2781 BP; 658 A; 678 C; 765 G; 680 T; 0 U; 0 Other;

Query Match 95.7%; Score 1783; DB 6; Length 2781;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Db	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCAATGGAGAA	360
Qy	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCTCTCTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTCCCTCTGCTCCTGAGATACTCTCTCTCTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTTAGGGAGTGCAGCCTTCAACATGTTTCATC	540

Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCGCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCGCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380

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Qy      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC 1440
        |||
Db      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC 1440

Qy      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
        |||
Db      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
        |||
Db      1501 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620
        |||
Db      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT 1620

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Db      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Db      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAG 1796

Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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RESULT 9
ABN83428

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ID      ABN83428 standard; cDNA; 2782 BP.
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AC      ABN83428;
XX
DT      21-AUG-2002 (first entry)
XX
DE      Human transporter protein coding sequence.
XX
KW      Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
KW      spleen; testis; leukocyte; foetal brain; chromosome 14; gene; ss.
XX
OS      Homo sapiens.
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FH      Key          Location/Qualifiers
FT      CDS          10. .2775
FT          /*tag= a
FT          /product= "Human transporter"
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PN      WO200233086-A2.
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PD      25-APR-2002.
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PF 17-OCT-2001; 2001WO-US032152.

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PR 17-OCT-2000; 2000US-0240836P.

PR 13-MAR-2001; 2001US-00804474.

XX

PA (PEKE) PE CORP NY.

XX

PI Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;

PI Beasley EM;

XX

DR WPI; 2002-479677/51.

DR P-PSDB; ABB83246.

XX

PT Human transporter peptide related to sodium/calcium exchanger subfamily

PT for identifying modulators useful for treating a disease or condition

PT mediated by human transporter protein.

XX

PS Claim 4; Fig 1; 200pp; English.

XX

CC The present sequence is the coding sequence of a human transporter

CC protein, which is related to the sodium/calcium exchanger subfamily.

CC Experimental data indicates expression of the transporter gene in humans

CC in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal

CC brain. The gene of the transporter was mapped to chromosome 14 by ePCR

XX

SQ Sequence 2782 BP; 655 A; 685 C; 766 G; 676 T; 0 U; 0 Other;

Query Match 95.7%; Score 1783; DB 6; Length 2782;

Best Local Similarity 98.4%; Pred. No. 0;

Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Qy     361 ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
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Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
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Qy	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
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KW antiparkinsonian; hypotensive; nootropic; antianaemic; anticonvulsant;
 KW cerebroprotective; cardiant; anti-HIV; human immunodeficiency virus;
 KW antiasthmatic; antiatherosclerotic; antigout; antiarteriosclerotic;
 KW hepatotropic; antiinflammatory; virucide; cytostatic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200246415-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 05-DEC-2001; 2001WO-US046963.
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 PR 08-DEC-2000; 2000US-0254303P.
 PR 15-DEC-2000; 2000US-0256190P.
 PR 21-DEC-2000; 2000US-0257504P.
 PR 12-JAN-2001; 2001US-0261546P.
 PR 19-JAN-2001; 2001US-0262832P.
 PR 26-JAN-2001; 2001US-0264377P.
 PR 02-FEB-2001; 2001US-0266019P.
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 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Lee EA, Baughn MR, Yue H, Ding L, Raumann BE, Hafalia AJA;
 PI Khan FA, Nguyen DB, Elliott VS, Ramkumar J, Walia NK, Ison CH;
 PI Lu Y, Gandhi AR, Warren BA, Duggan BM, Tribouley CM, Burford N;
 PI Lu DAM, Lal PG, Yao MG, Xu Y, Bruns CM, Thangavelu K, Swarnakar A;
 PI Tang YT, Azimzai Y, Thornton M, Arvizu C, Policky JL;
 XX
 DR WPI; 2002-519667/55.
 DR P-PSDB; ABP74104.
 XX
 PT Novel human transporter and ion channel polypeptide, useful in diagnosis,
 PT prevention or treatment of transport, neurological, muscle, immunological
 PT and cell proliferative disorders.
 XX
 PS Claim 96; SEQ ID NO 41; 146pp + Sequence Listing; English.
 XX
 CC The invention relates to human transporter and ion channel polypeptide
 CC (TRICH) (I) selected from one of 32 polypeptide sequences (ABP74096-
 CC ABP74127), a naturally occurring polypeptide comprising a sequence having
 CC at least sequence 90 % identity to (I) or a biologically active or
 CC immunogenic fragment of (I). (I) is useful for screening a compound for
 CC effectiveness as an agonist or antagonist, for screening a compound that
 CC specifically binds (I) or modulates the activity of (I) and for preparing
 CC a polyclonal or monoclonal antibody by hybridoma technology.
 CC Polynucleotides (II, ABZ33727-ABZ33758) encoding (I) are useful for
 CC screening a compound altering gene expression. (I) and (II) are useful in
 CC a diagnostic tests for a condition or a disease associated with the
 CC expression of TRICH in a biological sample, especially disorders selected
 CC from a transport disorder such as cystic fibrosis, diabetes mellitus,
 CC Parkinson's disease, cardiac disorders, neurological disorders such as
 CC Alzheimer's disease, Huntington's disease, muscle disorders,
 CC immunological disorder such as AIDS, asthma and atherosclerosis, and cell
 CC proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis and
 CC cancer. (II) is useful for creating knock-in humanised animals or
 CC transgenic animals to model human diseases, in somatic or germline gene

CC therapy, to generate a transcript image of a tissue or cell type, for
CC detecting differences in the chromosomal location due to translocation,
CC inversion among normal, carrier or affected individuals and for mapping
CC genomic sequences. Note: The sequence data for this patent is not
CC represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office

XX

SQ Sequence 2966 BP; 692 A; 725 C; 809 G; 740 T; 0 U; 0 Other;

Query Match 95.7%; Score 1783; DB 6; Length 2966;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Db      741 ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 800

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Qy	661	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
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Db	921	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	980
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	981	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1040
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCCATTTTCTAGATGGGAAC	900
Db	1041	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCCATTTTCTAGATGGGAAC	1100
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1101	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1160
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Db	1161	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1220
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1221	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCTTCTACCGTATCCAAGCCACTCGT	1280
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Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGATGAACACTTC	1440
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Db      1941 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1996
Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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RESULT 11

ABN83429

ID ABN83429 standard; DNA; 126512 BP.

XX

AC ABN83429;

XX

DT 21-AUG-2002 (first entry)

XX

DE Human transporter protein gene.

XX

KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;

KW spleen; testis; leukocyte; foetal brain; chromosome 14; gene;

KW single nucleotide polymorphism; SNP; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

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FT /standard_name= "Single nucleotide polymorphism"

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FT /standard_name= "Single nucleotide polymorphism"

FT /note= "This variation is an indel"

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FT CDS 2010..124505

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FT	variation	replace(71900,T)
FT		/*tag= bg
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	replace(71901,A)
FT		/*tag= bh
FT		/standard_name= "Single nucleotide polymorphism"
FT	variation	replace(72369,T)
FT		/*tag= bi

Query Match

95.7%; Score 1782.8; DB 6; Length 126512;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
      |||
Db    2010 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 2069

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
      |||
Db    2070 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 2129

Qy    121 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180
      |||
Db    2130 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 2189

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
      |||
Db    2190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 2249

Qy    241 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
      |||
Db    2250 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 2309

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
      |||
Db    2310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 2369

Qy    361 ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
      |||
Db    2370 ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 2429

Qy    421 CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 480
      |||
Db    2430 CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT 2489

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
      |||
Db    2490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 2549

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
      |||
Db    2550 ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 2609

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
      |||
Db    2610 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 2669

Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC 720
      |||
Db    2670 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC 2729

Qy    721 TTTCCAGTGTGTGTCTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
      |||
Db    2730 TTTCCAGTGTGTGTCTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 2789

Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
      |||
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Db	2790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	2849
Qy	841	CACCCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCCATTTTCTAGATGGGAAC	900
Db	2850	CACCCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCCATTTTCTAGATGGGAAC	2909
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	2910	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	2969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	2970	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	3029
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	3030	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	3089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1140
Db	3090	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	3149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	3150	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	3209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	3210	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	3269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	3270	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	3329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	3330	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	3389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	3390	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	3449
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	3450	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	3509
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	3510	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	3569
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	3570	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	3629
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	3630	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	3689

Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
 |||
 Db 3690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 3749

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGTAT 1786
 |||
 Db 3750 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGTGT 3795

RESULT 12

ABX56261

ID ABX56261 standard; DNA; 2813 BP.

XX

AC ABX56261;

XX

DT 19-FEB-2003 (first entry)

XX

DE Human NOV1a CG56258-01 DNA SEQ ID 1.

XX

KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
 KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease; ds.

XX

OS Homo sapiens.

XX

PN WO200281625-A2.

XX

PD 17-OCT-2002.

XX

PF 03-APR-2002; 2002WO-US010366.

XX

PR 03-APR-2001; 2001US-0281086P.

PR 05-APR-2001; 2001US-0281906P.

PR 06-APR-2001; 2001US-0282020P.

PR 10-APR-2001; 2001US-0282930P.

PR 12-APR-2001; 2001US-0283444P.

PR 12-APR-2001; 2001US-0283512P.

PR 13-APR-2001; 2001US-0283657P.

PR 13-APR-2001; 2001US-0283678P.

PR 13-APR-2001; 2001US-0283710P.

PR 17-APR-2001; 2001US-0284234P.

PR 19-APR-2001; 2001US-0285325P.

PR 20-APR-2001; 2001US-0285381P.

PR 24-APR-2001; 2001US-0286068P.

PR 25-APR-2001; 2001US-0286292P.

PR 07-JUN-2001; 2001US-0296692P.

PR 26-JUN-2001; 2001US-0300883P.

PR 08-AUG-2001; 2001US-0311003P.

PR 13-AUG-2001; 2001US-0311973P.

PR 16-AUG-2001; 2001US-0312901P.

PR 14-SEP-2001; 2001US-0322283P.

PR 05-OCT-2001; 2001US-0327448P.

Db	69	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	128
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	180
Db	129	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG	188
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	189	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	248
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	249	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	308
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	309	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	368
Qy	361	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	369	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	428
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	429	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	488
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	489	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	548
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	549	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	608
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	609	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	668
Qy	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	669	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	728
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	729	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	788
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	789	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	848
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	849	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	908
Qy	901	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	909	CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	968

Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	969	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1028
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1029	TACTATGCTCTTTCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT	1088
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1089	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1148
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1149	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1208
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1209	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1268
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1269	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1328
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1329	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1388
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Db	1389	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1448
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1449	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1508
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1509	GCAATATTCAACAGTCTTCCCTTGCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1568
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1569	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1628
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1629	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1688
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1689	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1748
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT	1784
Db	1749	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT	1792

RESULT 13

ABX56262

ID ABX56262 standard; DNA; 2840 BP.

XX

AC ABX56262;

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DT 19-FEB-2003 (first entry)

XX

DE Human NOV1b CG56558-02 DNA SEQ ID 3.

XX

KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;
KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW metabolic syndrome X; wasting disease; ds.

XX

OS Homo sapiens.

XX

PN WO200281625-A2.

XX

PD 17-OCT-2002.

XX

PF 03-APR-2002; 2002WO-US010366.

XX

PR 03-APR-2001; 2001US-0281086P.

PR 05-APR-2001; 2001US-0281906P.

PR 06-APR-2001; 2001US-0282020P.

PR 10-APR-2001; 2001US-0282930P.

PR 12-APR-2001; 2001US-0283444P.

PR 12-APR-2001; 2001US-0283512P.

PR 13-APR-2001; 2001US-0283657P.

PR 13-APR-2001; 2001US-0283678P.

PR 13-APR-2001; 2001US-0283710P.

PR 17-APR-2001; 2001US-0284234P.

PR 19-APR-2001; 2001US-0285325P.

PR 20-APR-2001; 2001US-0285381P.

PR 24-APR-2001; 2001US-0286068P.

PR 25-APR-2001; 2001US-0286292P.

PR 07-JUN-2001; 2001US-0296692P.

PR 26-JUN-2001; 2001US-0300883P.

PR 08-AUG-2001; 2001US-0311003P.

PR 13-AUG-2001; 2001US-0311973P.

PR 16-AUG-2001; 2001US-0312901P.

PR 14-SEP-2001; 2001US-0322283P.

PR 05-OCT-2001; 2001US-0327448P.

PR 31-DEC-2001; 2001US-0345734P.

PR 03-JAN-2002; 2002US-0345755P.

PR 04-FEB-2002; 2002US-0354391P.

PR 02-APR-2002; 2002US-00114153.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;

PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;

Qy	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	303	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	362
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	363	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	422
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	423	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	482
Qy	421	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTC	480
Db	483	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTC	542
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	543	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	602
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	603	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	662
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	663	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	722
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	723	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	782
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	783	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	842
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	843	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	902
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCTTTCTAGATGGGAAC	900
Db	903	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCTTTCTAGATGGGAAC	962
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	963	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1022
Qy	961	AAGGATCTGAAGCAAAAAACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1023	AAGGATCTGAAGCAAAAAACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1082
Qy	1021	TACTATGCTCTTTCCCAACAGAAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1083	TACTATGCTCTTTCCCAACAGAAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT	1142

Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1143	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1202
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1203	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1262
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1263	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1322
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1323	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1382
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTCTGAAGCCAGGAGAGACC	1380
Db	1383	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTCTGAAGCCAGGAGAGACC	1442
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1443	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1502
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1503	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1562
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1563	GCAATATTCAACAGTCTTCCCTTGCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1622
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1623	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1682
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1683	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1742
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1743	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1802
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT	1784
Db	1803	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT	1846

RESULT 14

ABX56263

ID ABX56263 standard; DNA; 2685 BP.

XX

AC ABX56263;

XX

DT 19-FEB-2003 (first entry)

XX

DE Human NOV1c 248057963 DNA SEQ ID 5.
 XX
 KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
 KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200281625-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010366.
 XX
 PR 03-APR-2001; 2001US-0281086P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 06-APR-2001; 2001US-0282020P.
 PR 10-APR-2001; 2001US-0282930P.
 PR 12-APR-2001; 2001US-0283444P.
 PR 12-APR-2001; 2001US-0283512P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285381P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 25-APR-2001; 2001US-0286292P.
 PR 07-JUN-2001; 2001US-0296692P.
 PR 26-JUN-2001; 2001US-0300883P.
 PR 08-AUG-2001; 2001US-0311003P.
 PR 13-AUG-2001; 2001US-0311973P.
 PR 16-AUG-2001; 2001US-0312901P.
 PR 14-SEP-2001; 2001US-0322283P.
 PR 05-OCT-2001; 2001US-0327448P.
 PR 31-DEC-2001; 2001US-0345734P.
 PR 03-JAN-2002; 2002US-0345755P.
 PR 04-FEB-2002; 2002US-0354391P.
 PR 02-APR-2002; 2002US-00114153.
 XX
 PA (CURA-) CURAGEN CORP.
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 PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
 PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
 PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
 PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
 PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
 PI Mazur A;
 XX
 DR WPI; 2003-046862/04.
 DR P-PSDB; ABU12043.
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 PT New isolated NOVX polypeptide useful for treating cardiomyopathy,

Qy	446	TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTA	505
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Qy	686	TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTCCAGTGTGTGTCCTTCTGGCCT	745
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Qy	866	GGAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAGGAAG	925
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Qy	1226	AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA	1285
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Qy	1286	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1345

Db	1202	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1261
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Qy	1406	TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1465
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Qy	1706	TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT	1765
Db	1622	TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT	1681
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AAD24450

ID AAD24450 standard; cDNA; 4087 BP.

XX

AC AAD24450;

XX

DT 07-MAY-2002 (first entry)

XX

DE Bovine NCX-1 cDNA.

XX

KW Bovine; recombinant protein; larvae expression system; membrane protein;
 KW transport protein; cardiac sodium-calcium exchange protein; Na-K ATPase;
 KW NCX1; cystic fibrosis transmembrane conductance regulator; CFTR; vaccine;
 KW channel forming protein; junctional protein; connexin 32; ss.

XX

OS Bos taurus.

XX

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FH   Key          Location/Qualifiers
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FT               /product= "Bovine NCX-1 protein"
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PN   WO200206464-A2.
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PD   24-JAN-2002.
XX
PF   09-JUL-2001; 2001WO-US021606.
XX
PR   13-JUL-2000; 2000US-0218125P.
XX
PA   (UMOR ) UNIV MISSOURI.
XX
PI   Hale CC, Price EM;
XX
DR   WPI; 2002-171806/22.
DR   P-PSDB; AAE18291.
XX
PT   Producing recombinant proteins e.g. membrane, transport and channel
PT   forming proteins in larvae expression system, by infecting larvae with
PT   vector having a sequence encoding recombinant fusion protein with
PT   affinity tag.
XX
PS   Example 1; Page 31-37; 40pp; English.
XX
CC   The patent discloses methods of producing recombinant proteins in larvae
CC   expression system, by infecting the larvae with vector having a sequence
CC   encoding recombinant fusion protein with affinity tag. The methods are
CC   useful for producing recombinant protein, preferably membrane proteins,
CC   transport proteins such as NCX1 (cardiac sodium-calcium exchange protein)
CC   or Na-K ATPase, channel forming proteins such as cystic fibrosis trans-
CC   membrane conductance regulator (CFTR), junctional protein (conexin 32),
CC   receptor, cytoskeletal and other membrane associated proteins. They are
CC   also useful for producing prostate specific membrane antigens and sodium
CC   phosphate co-transporters from kidney. The methods are also useful for
CC   producing recombinant fusion proteins in large quantities that are both
CC   highly homogenous and biologically active. The recombinant proteins
CC   produced by the methods of the invention can be included as part of a
CC   pharmaceutical, nutritional, drug or vaccine composition. The present
CC   sequence is a cDNA encoding bovine NCX-1 protein
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SQ   Sequence 4087 BP; 1057 A; 950 C; 1057 G; 1023 T; 0 U; 0 Other;

Query Match          43.5%; Score 810.6; DB 6; Length 4087;
Best Local Similarity 68.5%; Pred. No. 3.7e-242;
Matches 1211; Conservative 0; Mismatches 519; Indels 39; Gaps 5;

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Qy          106 GGGGACGTGCCAAGCACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAG 165
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Qy 346 AAACCCAATGGAGAAACCAGCACAAACCACTATTTCGGGTCTGGAATGAACTGTCTCCAAC 405
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Qy 406 CTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTG 465
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Qy 766 CTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATA 825
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Qy 826 GAGACAGAGGGTGACCACCC-----TAAGGGCATTGAGATGGATGGGAAAATGATG 876
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Qy 922 ---GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAA 978
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Qy	1099	AATATCCTGAAGAAACATGCAGCAGAACCAAGCAAGAAGGCCTCCAGCATGAGCGAGGTG	1158
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Db	1447	AACACGGAAGTGGCTGAAAATGACCCTGTCAGTAAGATCTTCTTTGAACAAGGGACATAT	1506
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Job time : 660.599 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 06:15:36 ; Search time 142.069 Seconds
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Title: US-10-054-680-3
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	44.8	2.4	2803	4	US-09-701-068-4	Sequence 4, Appli		
6	38.4	2.1	160	1	US-08-182-175A-44	Sequence 44, Appl		
7	38.4	2.1	160	1	US-08-474-633A-53	Sequence 53, Appl		
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	17	36.8	2.0	160	1	US-08-182-175A-34	Sequence 34, Appl
	18	36.8	2.0	160	1	US-08-474-633A-29	Sequence 29, Appl
	19	36.8	2.0	160	1	US-08-474-633A-31	Sequence 31, Appl
	20	36.8	2.0	160	4	US-08-823-771-29	Sequence 29, Appl
	21	36.8	2.0	160	4	US-08-823-771-31	Sequence 31, Appl
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	34	36	1.9	505	4	US-09-621-976-15639	Sequence 15639, A
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	39	35.6	1.9	231	3	US-09-461-697-207	Sequence 207, App
	40	35.6	1.9	282	3	US-09-461-697-205	Sequence 205, App
	41	35.6	1.9	306	3	US-09-461-697-203	Sequence 203, App
	42	35.6	1.9	696	3	US-09-461-697-193	Sequence 193, App
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	44	35.6	1.9	717	3	US-09-461-697-189	Sequence 189, App
	45	35.6	1.9	774	3	US-09-461-697-187	Sequence 187, App

ALIGNMENTS

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RESULT 1
US-09-701-068-3
; Sequence 3, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.
; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)..(1755)
US-09-701-068-3

Query Match 3.8%; Score 71.6; DB 4; Length 1935;
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Matches 268; Conservative 0; Mismatches 279; Indels 9; Gaps 2;

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Qy      226 AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCT 285
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Db      313 GCACGGTTCCTCAAGTCTATGGAGAATGTCGTGAAACATTCCCGTAAAGTGGTTACAATT 372

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Db      373 GATCCCATTACTAAAGCTGAAGTCATCACATACAAGAAAGTTTGGAACTTTACTATTGCA 432

Qy      403 AACCTGACCCTTATGGCCCTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAG 462
        || | | | |||| | || | || |||| | | || ||
Db      433 GACATCAGTTTGTGGCGTTTGGAACTAGCTTCCCTCAGATTCTTTGGCTACCATCGAT 492

Qy      463 GTGTGTGGTCAT-----GGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGG 516
        | | | | | | | | | | | | | | | | | | | |
Db      493 GCAATACGGAATATGGGGGAGCGGTATGCTGGAGGTCTTGGTCCTGGAACACTTGTTGGC 552

Qy      517 AGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGA 576
        || || || | | ||| |||| | | ||||| ||| || ||
Db      553 TCAGCTGCATTTGATCTTTTCCCCATCCACGCTGTTTGTGTGCTTGTGCCAAAAGCTGGA 612

Qy      577 GAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTT 636
        || | | |||| | || | || | | | | | | ||| |||
Db      613 GAACTGAAAAAGATATCCGACTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTTTGG 672

Qy      637 GCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGG 696
        || ||||| ||||| || || || || | || | || || ||
Db      673 GCTTACATCTGGCTATACATAATCCTCGAGGTGTGGTCACCAAACGTAATTACACTTGTG 732

Qy      697 GAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGAT 756
        || | | | || | | | | | | | | | | | | | |
Db      733 GAGGCATTATTGACAGTACTGCAATACGGATTGCTTCTAGTTCATGCGTACGCCCAAGAC 792

Qy      757 AAACGACTGCTCTTCT 772
        || ||| || | ||
Db      793 AAGCGATGGCCTTACT 808
```

RESULT 2

US-09-701-068-1

; Sequence 1, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.

; TITLE OF INVENTION: DNA CODING FOR A Mg²⁺/H⁺ OR Zn²⁺/H⁺ EXCHANGER AND
 TRANSGENIC PLANTS
 ; TITLE OF INVENTION: EXPRESSING SAME
 ; FILE REFERENCE: 01/21317
 ; CURRENT APPLICATION NUMBER: US/09/701,068
 ; CURRENT FILING DATE: 2001-05-07
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1950
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-701-068-1

Query Match 3.8%; Score 71.6; DB 4; Length 1950;
 Best Local Similarity 48.2%; Pred. No. 4.8e-12;
 Matches 268; Conservative 0; Mismatches 279; Indels 9; Gaps 2;

```

Qy      226 AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCT 285
        |||| | | ||||| | | || ||| || ||||| ||| ||
Db      258 AGGGGTGTGTTATATTTTCTCGGTCTTGCCTACTGCTTTATTGGGTTGTCAGCCATCACT 317

Qy      286 GACCGCTTCATGGCATCTATTG---AAGTCATCACCTCTCAAGAGAGGGAGGTGACAATT 342
        | || ||| | ||||| | ||| | | | | | | ||| |||||
Db      318 GCACGGTTCCTCAAGTCTATGGAGAATGTCGTGAAACATTCCCGTAAAGTGGTTACAATT 377

Qy      343 AAGAAACCCAATGGAGAAACCAGCACACCCTATTCGGGTCTGGAATGAAACTGTCTCC 402
        | | | | | || || || || | || |||| | || | |
Db      378 GATCCCATTACTAAAGCTGAAGTCATCACATACAAGAAAGTTTGGAACTTTACTATTGCA 437

Qy      403 AACCTGACCCTTATGGCCCTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAG 462
        || | | | |||| | || | ||| |||| | || || ||
Db      438 GACATCAGTTTGTGGCGTTTGGAACTAGCTTCCCTCAGATTTCTTTGGCTACCATCGAT 497

Qy      463 GTGTGTGGTCAT-----GGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGG 516
        | | | || | | ||||| | ||| || || || || || ||
Db      498 GCAATACGGAATATGGGGGAGCGGTATGCTGGAGGTCTTGGTCCTGGAACACTTGTGGC 557

Qy      517 AGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGA 576
        || || || | | ||| |||| | | ||||| ||| || |||
Db      558 TCAGCTGCATTTGATCTTTTCCCCATCCACGCTGTTTGTGTCGTTGTGCCAAAAGCTGGA 617

Qy      577 GAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTT 636
        || |||| | || | || | | | | || | || | || |
Db      618 GAACTGAAAAAGATATCCGACTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTGG 677

Qy      637 GCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGG 696
        || ||||| || || || || | || | || || || | || |
Db      678 GCTTACATCTGGCTATACATAATCCTCGAGGTGTGGTCACCAAACGTAATTACACTTGTG 737

Qy      697 GAAGGCCCTCCTCACTCTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGAT 756
        || | | | || | | | || | || | || | || | ||
Db      738 GAGGCATTATTGACAGTACTGCAATACGGATTGCTTCTAGTTCATGCGTACGCCCAAGAC 797

Qy      757 AAACGACTGCTCTTCT 772
        || || | || | ||
Db      798 AAGCGATGGCCTTACT 813
  
```

RESULT 3
 US-08-232-463-14
 ; Sequence 14, Application US/08232463
 ; Patent No. 5670367
 ; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEIFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232,463
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/935,313
 ; FILING DATE:
 ; APPLICATION NUMBER: EP 91 114 300.6
 ; FILING DATE: 26-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)836-9300
 ; TELEFAX: (703)683-4109
 ; TELEX: 899149
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7218 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: pTZgpt-Fls
 US-08-232-463-14

Query Match 2.8%; Score 51.6; DB 1; Length 7218;
 Best Local Similarity 5.9%; Pred. No. 2.7e-05;
 Matches 24; Conservative 215; Mismatches 169; Indels 0; Gaps 0;

Qy 395 CTGTCTCCAACCTGACCCCTTATGGCCCTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTT 454
 :: ::::: ::: ::::: : ::::: ::::: ::::: : :::::


```

Db      1078 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1137
Qy      455 TAATTGAGGTGTGTGGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTTGTAG 514
      :  ::      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      1138 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1197
Qy      515 GGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACG 574
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      1198 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1257
Qy      575 GAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCT 634
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      1258 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1317
Qy      635 TTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTT 694
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      1318 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1377
Qy      695 GGGAAGGCCTCCTCACTCTCTTCTTCTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAG 754
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      1378 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTA 1437
Qy      755 ATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAG 802
      |||  |  |||  ||  |||  |||  |  ||  |||
Db      1438 CCAAATTCTTCTATCTCTTTAACTACTTGCATAGATAGGTAATTACAG 1485

```

RESULT 4

US-08-232-463-14/c

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

```
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14
```

```
Query Match          2.7%; Score 51; DB 1; Length 7218;
Best Local Similarity 3.4%; Pred. No. 4.2e-05;
Matches 9; Conservative 161; Mismatches 91; Indels 0; Gaps 0;
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Qy      1603 GAATGTGATACTATTCATGTCTAGTGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGG 1662
        |||| || ||| : : : : : : : : : : : : : : : : : :
Db      1445 GAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1386

Qy      1663 ACATCAGGTGCCCCGGGGTACAGTCATCGTCCCCCTTTAGGACAGTAGAAGGGACAGCCAAG 1722
        : : : : : : : : : : : : : : : : : : : : : : :
Db      1385 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1326

Qy      1723 GGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACT 1782
        : : : : : : : : : : : : : : : : : : : : : : :
Db      1325 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1266

Qy      1783 GTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGAT 1842
        : : : : : : : : : : : : : : : : : : : : : : :
Db      1265 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1206

Qy      1843 GGGAAAGCCAGTATTGGGTGA 1863
        : : : : : : : : : : : : : : : : : : : : : : :
Db      1205 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1185
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RESULT 5

US-09-701-068-4

; Sequence 4, Application US/09701068

; Patent No. 6677506

; GENERAL INFORMATION:

; APPLICANT: Galil, Gad et al.

; TITLE OF INVENTION: DNA CODING FOR A Mg²⁺/H⁺ OR Zn²⁺/H⁺ EXCHANGER AND
TRANSGENIC PLANTS

; TITLE OF INVENTION: EXPRESSING SAME

; FILE REFERENCE: 01/21317

; CURRENT APPLICATION NUMBER: US/09/701,068

; CURRENT FILING DATE: 2001-05-07

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 2803
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-701-068-4

Query Match 2.4%; Score 44.8; DB 4; Length 2803;
Best Local Similarity 52.1%; Pred. No. 0.0021;
Matches 100; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Qy 477 GTTCATTGCTGGTGATCTGGGACCTTCTACCATTTGTAGGGAGTGCAGCCTTCAACATGTT 536
||| | | | ||| || ||| || ||| || | | ||
Db 950 GTTTTGT CATATAGGTCTTGGTCCTGGAACACTTGTGGCTCAGCTGCATTTGATCTTTT 1009

Qy 537 CATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCA 596
| |||| | | ||||| ||| || |||| | |||| |
Db 1010 CCCCATCCACGCTGTTTGTGTCTGTTGTGCCAAAAGCTGGAGAACTGAAAAAGATATCCGA 1069

Qy 597 TCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATAT 656
|| ||| | | | | ||| || | ||| ||||| || ||
Db 1070 CTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTGGGCTTACATCTGGCTATACAT 1129

Qy 657 GATTCTGGCAGT 668
|| || | ||
Db 1130 AATCCTCGAGGT 1141

RESULT 6

US-08-182-175A-44

; Sequence 44, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure
Containing Pro
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006

```

; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: E. coli
; CELL TYPE: DH5 alpha
; IMMEDIATE SOURCE:
; CLONE: 82-4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..151
; OTHER INFORMATION: /function= "synthetic storage protein"
; OTHER INFORMATION: /product= "protein"
; OTHER INFORMATION: /gene= "ssp"
; OTHER INFORMATION: /standard_name= "7.7.7.7.7.5"
US-08-182-175A-44

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Query Match          2.1%; Score 38.4; DB 1; Length 160;
Best Local Similarity 53.3%; Pred. No. 0.032;
Matches 81; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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Qy      1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
          | ||| ||| | || | || | || | || || | || |
Db          4 GGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGC 63

Qy      1768 AAGAATGATGAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
          | | ||| ||| | || | || | || || || | || | ||
Db          64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123

Qy      1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
          | ||| | |||| | || | || | ||
Db          124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155

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RESULT 7

US-08-474-633A-53

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; Sequence 53, Application US/08474633A
; Patent No. 5773691
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; APPLICANT: COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND
; TITLE OF INVENTION: METHODS FOR INCREASING
; TITLE OF INVENTION: INCREASING THE LYSINE

```

```

; TITLE OF INVENTION:  AND THREONINE CONTENT
; TITLE OF INVENTION:  OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES:  107
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  E. I. DU PONT DE NEMOURS
;   ADDRESSEE:  AND COMPANY
;   STREET:  1007 MARKET STREET
;   CITY:  WILMINGTON
;   STATE:  DELAWARE
;   COUNTRY:  U.S.A.
;   ZIP:  19898
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  FLOPPY DISK
;   COMPUTER:  IBM PC COMPATIBLE
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/474,633A
;   FILING DATE:
;   CLASSIFICATION:  800
; ATTORNEY/AGENT INFORMATION:
;   NAME:  BARBARA C. SIEGELL
;   REGISTRATION NUMBER:  30,684
;   REFERENCE/DOCKET NUMBER:  BB-1037-C
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  302-992-4931
;   TELEFAX:  302-773-0164
;   TELEX:  835420
; INFORMATION FOR SEQ ID NO:  53:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  160 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  DNA (genomic)
;   ORIGINAL SOURCE:
;     STRAIN:  E. coli
;     CELL TYPE:  DH5 alpha
;   IMMEDIATE SOURCE:
;     CLONE:  82-4
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  2..151
;     OTHER INFORMATION:  /function= "synthetic"
;     OTHER INFORMATION:  storage protein
;     OTHER INFORMATION:  /product= "protein"
;     OTHER INFORMATION:  /gene= "ssp"
;     OTHER INFORMATION:  /standard name=
;     OTHER INFORMATION:  "7.7.7.7.7.5"
US-08-474-633A-53

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Query Match          2.1%;  Score 38.4;  DB 1;  Length 160;
Best Local Similarity 53.3%;  Pred. No. 0.032;
Matches 81;  Conservative 0;  Mismatches 71;  Indels 0;  Gaps 0;

```

```

Qy      1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
          | |||  |||  | || |  || |  ||  ||||| |  || ||  |||  |

```

Db 4 GGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGC 63
 QY 1768 AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
 | | | | | | | | | | | | | | | | | | | | | |
 Db 64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123
 QY 1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
 | | | | | | | | | | | | | | | | | |
 Db 124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155

RESULT 8

US-08-823-771-53

; Sequence 53, Application US/08823771

; Patent No. 6459019

; GENERAL INFORMATION:

APPLICANT: E. I. DU PONT DE NEMOURS AND

: COMPANY

10 TITLE OF INVENTION: CHIMERIC GENES AND

METHODS FOR INCREASING

; INCREASING THE LYSINE

AND THREONINE CONTENT

```

; NUMBER OF SEQUENCES: 107

```

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS

AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

; STATE: DELAWARE

COUNTRY: U.S.A.

; ZIP: 19898

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: FLOPPY DISK
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;          COMPUTER: IBM PC COMPATIBLE

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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: MICROSOFT WORD VERSION 2.0C

```

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/823,771

FILING DATE: 24-Mar-1997

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/474,633

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

NAME: BARBARA C. SIEGELL

; REGISTRATION NUMBER: 30,684

REFERENCE/DOCKET NUMBER: BB-1037-C

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-992-4931

; TELEFAX: 302-773-0164

TELEX: 835420

; INFORMATION FOR SEQ ID NO: 53:

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; SEQUENCE CHARACTERISTICS:

```

LENGTH: 160 base pairs

```

;          TYPE: nucleic acid

```

```
; STRANDEDNESS: double
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;          TOPOLOGY: linear

```

```

; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: E. coli
; CELL TYPE: DH5 alpha
; IMMEDIATE SOURCE:
; CLONE: 82-4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..151
; OTHER INFORMATION: /function= "synthetic
; storage protein
; /product= "protein"
; /gene= "ssp"
; /standard name=
; "7.7.7.7.7.5"
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-08-823-771-53

```

```

Query Match          2.1%; Score 38.4; DB 4; Length 160;
Best Local Similarity 53.3%; Pred. No. 0.032;
Matches 81; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

```

```

QY      1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
          | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db        4 GGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGC 63

QY      1768 AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
          | | | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db        64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123

QY      1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
          | ||| | |||| | ||| | ||| |||
Db       124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155

```

RESULT 9

PCT-US92-06412-44

; Sequence 44, Application PC/TUS9206412

; GENERAL INFORMATION:

; APPLICANT: Saverio Carl Falco

; APPLICANT: Sharon J. Keeler

; APPLICANT: Janet A. Rice

; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure

Containing Pro

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh System, 6.0

; SOFTWARE: Microsoft Word, 4.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axaemethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: E. coli
; CELL TYPE: DH5 alpha
; IMMEDIATE SOURCE:
; CLONE: 82-4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..151
; OTHER INFORMATION: /function= "synthetic storage protein"
; OTHER INFORMATION: /product= "protein"
; OTHER INFORMATION: /gene= "ssp"
; OTHER INFORMATION: /standard_name= "7.7.7.7.7.5"
PCT-US92-06412-44

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Query Match          2.1%; Score 38.4; DB 5; Length 160;
Best Local Similarity 53.3%; Pred. No. 0.032;
Matches 81; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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Qy      1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
          | ||| ||| | || | || | ||| | || || ||| |
Db      4 GGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGC 63

Qy      1768 AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
          | | ||| ||| | || | || ||||| | || ||| || ||
Db      64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123

Qy      1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
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Db      124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155

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RESULT 10
US-09-310-463-3/c
; Sequence 3, Application US/09310463A
; Patent No. 6384203

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; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Borges, Luis
; TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte
Immunoglobulin-
; TITLE OF INVENTION: Like Receptors (LIR)
; FILE REFERENCE: 2624-A
; CURRENT APPLICATION NUMBER: US/09/310,463A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 08/842,248
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2777
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (168)..(2126)
US-09-310-463-3
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Best Local Similarity 49.0%; Pred. No. 0.23;
Matches 102; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
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Qy      1363 CTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTT 1422
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Db      220 CTGGGGCCCAGACTCAGCCCGAGACAGATCAGGACCGTGAGGATGGGGGTTCATGGCGTCT 161

Qy      1423 GAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCA 1482
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Db      160 CCTCCCACTGCCCTGCTCTGTGGATGGATGAGCCCTCGGTGCATGGCAGTCGTCCCTCCA 101

Qy      1483 GAGGAGGGGATGCCTCCAGCAATATTTCA 1510
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RESULT 11

US-08-842-248A-3/c

; Sequence 3, Application US/08842248A

; Patent No. 6448035

; GENERAL INFORMATION:

; APPLICANT: Cosman, David J.

; TITLE OF INVENTION: Family of Immunoregulators Designated

; TITLE OF INVENTION: Leukocyte Immunoglobulin-Like Receptors (LIR)

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Janis C. Henry, Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

```

; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM/PC Compatible
; OPERATING SYSTEM: Microsoft Word 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,248A
; FILING DATE: April 24, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C.
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: 18a3
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 168..2123
US-08-842-248A-3

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Query Match          2.1%; Score 38.4; DB 4; Length 2777;
Best Local Similarity 49.0%; Pred. No. 0.23;
Matches 102; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

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Qy      1303 ACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTT 1362
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Db      280 ACAGAGCCTGGTTCAGCCCAGAGGGTGGGCTTGGGGAGGTGCCCTGCCTGCACGTGGGTC 221

Qy      1363 CTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTT 1422
          |||  |||  ||  |  ||  ||  ||  ||  |  |  ||  |  |  |  |
Db      220 CTGGGGCCCAGACTCAGCCCAGACAGATCAGGACCGTGAGGATGGGGTCATGGCGTCT 161

Qy      1423 GAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCA 1482
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Qy      1483 GAGGAGGGGATGCCTCCAGCAATATTCA 1510
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Db      100 GCCCTGGAGATGCTTCAGGGAAGACCCA 73

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RESULT 12
US-09-007-005-17/c

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; Sequence 17, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

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Query Match          2.0%; Score 37.4; DB 3; Length 289;
Best Local Similarity 6.5%; Pred. No. 0.1;
Matches 14; Conservative 93; Mismatches 108; Indels 0; Gaps 0;

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Db      225 YCYTYGYSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYN 166

Qy      668 TCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTCCAG 727
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Db      165 YSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYN 106

Qy      728 TGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACA 787
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Db      105 YSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYNSYNYN 46
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Db      45 YAYAYTYTYGYTYAYAYTYAYGYTYAYAYTYTY 11

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RESULT 13

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US-09-244-796-17/c
; Sequence 17, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.

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; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350007
; CURRENT APPLICATION NUMBER: US/09/244,796
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 289
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Translation template
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(289)
;   OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
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RESULT 14
US-09-148-545-110/c
; Sequence 110, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04

; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,618
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; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
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; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
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; EARLIER APPLICATION NUMBER: 60/056,882
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; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,880
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; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
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; EARLIER APPLICATION NUMBER: 60/047,589
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; EARLIER APPLICATION NUMBER: 60/047,614
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; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 110
; LENGTH: 1320
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Query Match          2.0%; Score 37.2; DB 4; Length 1320;
Best Local Similarity 47.7%; Pred. No. 0.33;
Matches 105; Conservative 1; Mismatches 114; Indels 0; Gaps 0;
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Qy      554 GTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCA 613
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Db      810 GTGTCAACGTCATCCCAGCCACGGCTGCTCGCCCCAGGTGACAGTGTGGCAGCTGAAGTC 751

Qy      614 TCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCT 673
        || | |||| | | | || | | | | | | | |
Db      750 TCCCGGCTGCCAGGGCTCACTTCCAAGCTTACAGAACTCGTGTCACTCATTGTGTGTCAGCT 691

Qy      674 CCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTG 733
        || || | || || | ||||| || | | ||||| | ||
Db      690 CCTGTGCCATCCACCTGGGTGTCAATGGCCTCCACAAGCCCCGCCATTTCCACTCTGTC 631

Qy      734 TCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTA 773
        ||||| | || || | ||| :| | |
Db      630 TCCTTCATCTCAGGCACATAGAAGTCTCCCTGCCSTGCCA 591
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RESULT 15

US-08-935-855-19/c

; Sequence 19, Application US/08935855

; Patent No. 6066485

; GENERAL INFORMATION:

; APPLICANT: Guthridge, Mark

; APPLICANT: Basilico, Claudio

; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE

; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th

; STREET: Floor


```

;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/935,855
;      FILING DATE:
;      CLASSIFICATION:  435
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1049-1-002 CIP
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;      INFORMATION FOR SEQ ID NO:  19:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  1890 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  cDNA
;      HYPOTHETICAL:  NO
;      ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-08-935-855-19

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Query Match          2.0%;  Score 37;  DB 3;  Length 1890;
Best Local Similarity 53.9%;  Pred. No. 0.49;
Matches  76;  Conservative  0;  Mismatches  65;  Indels  0;  Gaps  0;

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Qy      582 TCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTA 641
          || | | | | | | | | | | | | | | | | | | | | | |
Db      949 TCCCTGGCACCATCATCTCTTCTTCTTCTTCTTCATCGTCCTCTTCAGCCTCCTCGGTGT 890

Qy      642 CATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGG 701
          || | | | | | | | | | | | | | | | | | | | | |
Db      889 CATCCTCATCTTCCTCATTCCTCTGCCTCCTCACTGCTGTAGCCATCCTCTTCCTCGCTGC 830

Qy      702 CTCCTCACTCTCTTCTTCTT 722
          || | | | | | | | | | | | |
Db      829 ATTCCTCACTGTCTTCCTCTT 809

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Search completed: June 25, 2004, 15:37:22
Job time : 143.069 secs

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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 07:13:27 ; Search time 753.008 Seconds
(without alignments)
11333.972 Million cell updates/sec

Title: US-10-054-680-3
Perfect score: 1863
Sequence: 1 atggcgtgggttaaggttgca.....ggaaagccagtattgggtga 1863

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

No.	Score	Match	Length	DB	ID	Description
1	1863	100.0	1863	14	US-10-054-680-3	Sequence 3, Appli
2	1784.6	95.8	2766	14	US-10-054-680-1	Sequence 1, Appli
3	1784.6	95.8	3812	14	US-10-054-680-5	Sequence 5, Appli
4	1784.4	95.8	2534	15	US-10-256-537-1	Sequence 1, Appli
5	1784.4	95.8	2534	15	US-10-256-537-3	Sequence 3, Appli
6	1783	95.7	2781	15	US-10-275-116-1	Sequence 1, Appli
7	1783	95.7	2782	9	US-09-804-474A-1	Sequence 1, Appli
8	1782.8	95.7	126512	9	US-09-804-474A-3	Sequence 3, Appli
9	1782.4	95.7	2813	15	US-10-114-153-1	Sequence 1, Appli
10	1782.4	95.7	2840	15	US-10-114-153-3	Sequence 3, Appli
11	1694.8	91.0	2685	15	US-10-114-153-5	Sequence 5, Appli
12	821.4	44.1	823	15	US-10-029-386-20265	Sequence 20265, A
13	810.6	43.5	4087	9	US-09-901-419-1	Sequence 1, Appli
14	785.2	42.1	1836	9	US-09-864-761-16939	Sequence 16939, A
15	783.2	42.0	6106	16	US-10-062-674-1648	Sequence 1648, Ap
16	713.4	38.3	3004	16	US-10-388-934-506	Sequence 506, App
17	692.4	37.2	4282	15	US-10-281-866-1	Sequence 1, Appli
18	692.4	37.2	4282	15	US-10-281-866-3	Sequence 3, Appli
19	503.4	27.0	505	15	US-10-029-386-6536	Sequence 6536, Ap
20	494	26.5	551	15	US-10-029-386-4103	Sequence 4103, Ap
21	366	19.6	366	15	US-10-029-386-17804	Sequence 17804, A
22	334.4	17.9	507	15	US-10-029-386-4003	Sequence 4003, Ap
23	180	9.7	180	15	US-10-029-386-17706	Sequence 17706, A
24	164.2	8.8	459	9	US-09-864-761-102	Sequence 102, App
25	146.6	7.9	1132	16	US-10-369-493-30006	Sequence 30006, A
26	91.4	4.9	1792	16	US-10-369-493-29835	Sequence 29835, A
27	79	4.2	477	10	US-09-918-995-2005	Sequence 2005, Ap
28	79	4.2	1187	13	US-10-243-552-809	Sequence 809, App
29	71.6	3.8	1617	9	US-09-938-842A-2591	Sequence 2591, Ap
30	71.6	3.8	1617	11	US-09-938-842A-2591	Sequence 2591, Ap
31	58.2	3.1	862	13	US-10-424-599-86000	Sequence 86000, A
32	39.6	2.1	1635	13	US-10-282-122A-29169	Sequence 29169, A
33	39.6	2.1	30306	13	US-10-087-192-523	Sequence 523, App
34	38.6	2.1	750	13	US-10-027-632-18725	Sequence 18725, A
35	38.6	2.1	750	16	US-10-027-632-18725	Sequence 18725, A
36	38.4	2.1	160	15	US-10-023-066A-53	Sequence 53, Appl
c 37	38.4	2.1	2777	15	US-10-139-662-3	Sequence 3, Appli
c 38	38.4	2.1	2777	15	US-10-139-683-3	Sequence 3, Appli
c 39	38.4	2.1	2777	15	US-10-143-618-3	Sequence 3, Appli
c 40	38.4	2.1	2897	13	US-10-240-425-366	Sequence 366, App
41	37.8	2.0	1566	13	US-10-424-599-77447	Sequence 77447, A
42	37.8	2.0	1638	13	US-10-282-122A-29556	Sequence 29556, A
43	37.4	2.0	1504	9	US-09-822-849A-214	Sequence 214, App
c 44	37.4	2.0	2946	16	US-10-369-493-33761	Sequence 33761, A
45	37.2	2.0	903	13	US-10-424-599-131200	Sequence 131200,

ALIGNMENTS

RESULT 1
 US-10-054-680-3
 ; Sequence 3, Application US/10054680
 ; Publication No. US20020132998A1
 ; GENERAL INFORMATION:

```

; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and
Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0301-USA
; CURRENT APPLICATION NUMBER: US/10/054,680
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,384
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-680-3

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Query Match          100.0%; Score 1863; DB 14; Length 1863;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1863; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGGTGTCATCCTG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGGTGTCATCCTG 180

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy    241 TTTGTGGCCCTGATATACATGTTTCCTTGGGGGTGCCATCATTGCTGACCGCTTCATGGCA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGTGGCCCTGATATACATGTTTCCTTGGGGGTGCCATCATTGCTGACCGCTTCATGGCA 300

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy    361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy    421 CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540

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Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCCAACAGAAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCCAACAGAAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380

Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Db	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT	1680
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGTATGTGACAGACAGGAA	1800
Db	1741	GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAACTGTATGTGACAGACAGGAA	1800
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG	1860
Db	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG	1860
Qy	1861	TGA	1863
Db	1861	TGA	1863

RESULT 2

US-10-054-680-1

; Sequence 1, Application US/10054680

; Publication No. US20020132998A1

; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan

; APPLICANT: Hilbun, Erin

; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and Polynucleotides Encoding the

; TITLE OF INVENTION: Same

; FILE REFERENCE: LEX-0301-USA

; CURRENT APPLICATION NUMBER: US/10/054,680

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/263,384

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2766

; TYPE: DNA

; ORGANISM: homo sapiens
US-10-054-680-1

Query Match 95.8%; Score 1784.6; DB 14; Length 2766;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Qy	121	ACAGGGCAGAACAAATGAGTCTCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Db	121	ACAGGGCAGAACAAATGAGTCTCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG	180
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Qy	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Db	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCCTTATGGCC	420
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780

Db	721	TTTCCAGTGTGTGTCTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCTTGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCTTGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCCAACAGAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCCAACAGAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Qy	1321	AATGCAGGGGCTGACTATGAGTTACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1321	AATGCAGGGGCTGACTATGAGTTACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620


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Qy      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
          |||
Db      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680

Qy      1681 ACAGTCATCGTCCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
          |||
Db      1681 ACAGTCATCGTCCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAACTGTATGTGACAGACAGGAA 1800
          |||
Db      1741 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
          |||
Db      1797 GGTTAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837

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RESULT 3

US-10-054-680-5

; Sequence 5, Application US/10054680

; Publication No. US20020132998A1

; GENERAL INFORMATION:

; APPLICANT: Friddle, Carl Johan

; APPLICANT: Hilbun, Erin

; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and Polynucleotides Encoding the

; TITLE OF INVENTION: Same

; FILE REFERENCE: LEX-0301-USA

; CURRENT APPLICATION NUMBER: US/10/054,680

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/263,384

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 3812

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-054-680-5

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Query Match          95.8%; Score 1784.6; DB 14; Length 3812;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
          |||
Db      618 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 677

Qy      61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
          |||
Db      678 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 737

Qy      121 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 180
          |||
Db      738 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 797

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Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	798	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	857
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	858	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	917
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	918	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	977
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	978	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	1037
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	1038	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	1097
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	1098	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	1157
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	1158	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	1217
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	1218	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1277
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1278	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1337
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1338	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1397
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1398	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1457
Qy	841	CACCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1458	CACCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1517
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1518	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1577
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1578	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1637
Qy	1021	TACTATGCTCTTTCCCAACAGAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080

Db	1638	 TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1697
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1698	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1757
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1758	 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1817
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1818	 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1877
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1878	 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1937
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1938	 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1997
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1998	 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	2057
Qy	1441	TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	2058	 TTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	2117
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	2118	 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	2177
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	2178	 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	2237
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	2238	 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	2297
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	2298	 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	2357
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA	1800
Db	2358	 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG	2413
Qy	1801	GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA	1841
Db	2414	 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA	2454

US-10-256-537-1
; Sequence 1, Application US/10256537
; Publication No. US20030162196A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN
; TITLE OF INVENTION: NA/CA EXCHANGER FAMILY MEMBER
; FILE REFERENCE: MPI01-231P1RM
; CURRENT APPLICATION NUMBER: US/10/256,537
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/325,737
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2534
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-256-537-1

Query Match 95.8%; Score 1784.4; DB 15; Length 2534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	343	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	402
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	403	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	462
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	463	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	522
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	523	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	582
Qy	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	300
Db	583	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCATCATTGCTGACCGCTTCATGGCA	642
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	643	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	702
Qy	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	703	ACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	762
Qy	421	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	763	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTAATTGAGGTGTGTGGTCATGGGTTC	822
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540

Db	823		ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	882
Qy	541		ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	883		ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	942
Qy	601		CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	943		CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	1002
Qy	661		CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	1003		CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	1062
Qy	721		TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	1063		TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	1122
Qy	781		ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	1123		ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	1182
Qy	841		CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	1183		CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	1242
Qy	901		CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1243		CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1302
Qy	961		AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1303		AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1362
Qy	1021		TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1363		TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1422
Qy	1081		ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1423		ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1482
Qy	1141		TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1483		TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1542
Qy	1201		GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1543		GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1602
Qy	1261		AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1603		AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1662
Qy	1321		AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380

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Db      1663 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1722
Qy      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC 1440
        |||
Db      1723 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC 1782
Qy      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
        |||
Db      1783 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1842
Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1560
        |||
Db      1843 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1902
Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
        |||
Db      1903 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1962
Qy      1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
        |||
Db      1963 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 2022
Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
        |||
Db      2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082
Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
        |||
Db      2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128

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RESULT 5

US-10-256-537-3

; Sequence 3, Application US/10256537

; Publication No. US20030162196A1

; GENERAL INFORMATION:

; APPLICANT: Carroll, Joseph M.

; TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN

; TITLE OF INVENTION: NA/CA EXCHANGER FAMILY MEMBER

; FILE REFERENCE: MPI01-231P1RM

; CURRENT APPLICATION NUMBER: US/10/256,537

; CURRENT FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: 60/325,737

; PRIOR FILING DATE: 2001-09-28

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 2534

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (343)...(2130)

US-10-256-537-3

Query Match 95.8%; Score 1784.4; DB 15; Length 2534;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
      |||
Db     343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
      |||
Db     403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 180
      |||
Db     463 ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCTATCCTG 522

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
      |||
Db     523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy    241 TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
      |||
Db     583 TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
      |||
Db     643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy    361 ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
      |||
Db     703 ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy    421 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTC 480
      |||
Db     763 CTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTC 822

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
      |||
Db     823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 882

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
      |||
Db     883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
      |||
Db     943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
      |||
Db    1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062

Qy    721 TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
      |||
Db   1063 TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1122

Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
      |||
Db   1123 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1182
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Qy	841	CACCCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	900
Db	1183	CACCCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTTCCATTTTCTAGATGGGAAC	1242
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	1243	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1302
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1303	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1362
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1363	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1422
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1423	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1482
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1483	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1542
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1543	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1602
Qy	1261	AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1603	AAAGGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1662
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1663	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1722
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440
Db	1723	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1782
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1783	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1842
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	1843	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCCTAGCCTCCCCTTGTGTGGCCACA	1902
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1620
Db	1903	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCAT	1962
Qy	1621	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	1963	GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT	2022


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Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
          |||
Db      2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
          |||
Db      2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128

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RESULT 6

US-10-275-116-1

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; Sequence 1, Application US/10275116
; Publication No. US20030096312A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: No. US20030096312A1el natrium-calcium exchanger protein
; FILE REFERENCE: HNCX3CWWS
; CURRENT APPLICATION NUMBER: US/10/275,116
; CURRENT FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2781)
US-10-275-116-1

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Query Match          95.7%; Score 1783; DB 15; Length 2781;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
          |||
Db      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy      61 TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
          |||
Db      61 TTTGTGCTCTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 180
          |||
Db      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTTCATCCTG 180

Qy      181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
          |||
Db      181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy      241 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
          |||
Db      241 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy      301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
          |||
Db      301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

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Qy	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	361	ACCAGCACAACTACTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Db	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC	480
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Qy	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	661	CTGGCAGTCTTCTCCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Qy	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1021	TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200

Qy 1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
 |||
 Db 1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy 1261 AAAGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
 |||
 Db 1261 AAAGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
 |||
 Db 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC 1440
 |||
 Db 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC 1440

Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
 |||
 Db 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCCTAGCCTCCCCTTGTGTGGCCACA 1560
 |||
 Db 1501 GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
 |||
 Db 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy 1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
 |||
 Db 1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680

Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
 |||
 Db 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA 1800
 |||
 Db 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy 1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
 |||
 Db 1797 GGTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837

RESULT 7

US-09-804-474A-1

; Sequence 1, Application US/09804474A

; Patent No. US20020119518A1

; GENERAL INFORMATION:

; APPLICANT: KODET, Stefan et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000891

; CURRENT APPLICATION NUMBER: US/09/804,474A

; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2782
; TYPE: DNA
; ORGANISM: Human
US-09-804-474A-1

Query Match 95.7%; Score 1783; DB 9; Length 2782;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

Qy	1	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	60
Db	10	ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC	69
Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	70	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	129
Qy	121	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	180
Db	130	ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG	189
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	190	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	249
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGCCATCATTGCTGACCGCTTCATGGCA	300
Db	250	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGCCATCATTGCTGACCGCTTCATGGCA	309
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	369
Qy	361	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	370	ACCAGCACAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	429
Qy	421	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	430	CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTTGAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	490	ATTGCTGGTGATCTGGGACCTTCTACCATTTGAGGGAGTGCAGCCTTCAACATGTTTCATC	549
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	550	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	609
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	610	CGAGTCTTCTTCATCACCGCTGCTTGAGTATCTTTGCCTACATCTGGCTCTATATGATT	669

Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	670	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	729
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	730	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	849
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCTATTTCTAGATGGGAAC	900
Db	850	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCTATTTCTAGATGGGAAC	909
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	910	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATCCTC	969
Qy	961	AAGGATCTGAAGCAAAAAACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAAT	1020
Db	970	AAGGATCTGAAGCAAAAAACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAAT	1029
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1030	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1090	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1150	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1210	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1270	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1330	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1440
Db	1390	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGGAGGAGGATGAACACTTC	1449
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1450	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1509
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA	1560

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Db      1510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCTTGTGTGGCCACA 1569
Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACCTTTTGAATGTGATACTATTCAT 1620
Db      1570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACCTTTTGAATGTGATACTATTCAT 1629
Qy      1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
Db      1630 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1689
Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
Db      1690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1749
Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAACTGTATGTGACAGACAGGAA 1800
Db      1750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1805
Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
Db      1806 GGT'AAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1846

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RESULT 8

US-09-804-474A-3

; Sequence 3, Application US/09804474A

; Patent No. US20020119518A1

; GENERAL INFORMATION:

; APPLICANT: KODET, Stefan et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000891

; CURRENT APPLICATION NUMBER: US/09/804,474A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 126512

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(126512)

; OTHER INFORMATION: n = A,T,C or G

US-09-804-474A-3

Query Match 95.7%; Score 1782.8; DB 9; Length 126512;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
Db      2010 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 2069

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Qy	61	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	120
Db	2070	TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC	2129
Qy	121	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG	180
Db	2130	ACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG	2189
Qy	181	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	240
Db	2190	CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	2249
Qy	241	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	2250	TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	2309
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	2310	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	2369
Qy	361	ACCAGCACAACCCTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	2370	ACCAGCACAACAACCTATTCGGGTCTGGAATGAACTGTCTCCAACCTGACCCTTATGGCC	2429
Qy	421	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	2430	CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	2489
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	2490	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	2549
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	2550	ATCATTGGCATCTGTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	2609
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	2610	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	2669
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	2670	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	2729
Qy	721	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	2730	TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	2789
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	2790	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	2849
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	2850	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	2909
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960

Db	2910	 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	2969
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	2970	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	3029
Qy	1021	TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	3030	 TACTATGCTCTTTCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	3089
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	3090	 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	3149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	3150	 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	3209
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	3210	 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	3269
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	3270	 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	3329
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	3330	 AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	3389
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTTGAGGAGGATGAACACTTC	1440
Db	3390	 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTTGAGGAGGATGAACACTTC	3449
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	3450	 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	3509
Qy	1501	GCAATATTCACAGTCTTCCCTTGCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	1560
Db	3510	 GCAATATTCACAGTCTTCCCTTGCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA	3569
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	3570	 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	3629
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTCTGCGGACATCAGGTGCCCGGGGT	1680
Db	3630	 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTCTGCGGACATCAGGTGCCCGGGGT	3689
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	3690	 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	3749
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT	1786

RESULT 9

US-10-114-153-1

; Sequence 1, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Shenoy, Suresh

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter

; APPLICANT: Smithson, Glennda

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gerlach, Valerie

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; APPLICANT: Li, Li

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Tchernev, Velizar

; APPLICANT: Gangolli, Esha

; APPLICANT: Vernet, Corine

; APPLICANT: Spytek, Kimberly

; APPLICANT: Malyankar, Uriel

; APPLICANT: Patturajan, Meera

; APPLICANT: Miller, Charles

; APPLICANT: Taupier, Raymond J. Jr.

; APPLICANT: Heyes, Melvyn

; APPLICANT: Ju, Jingfang

; APPLICANT: Peyman, John

; APPLICANT: Catterton, Elina

; APPLICANT: MacDougall, John

; APPLICANT: Edinger, Shlomit

; APPLICANT: Stone, David

; APPLICANT: Mazur, Ann

; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS

; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE

; FILE REFERENCE: 21402-322A

; CURRENT APPLICATION NUMBER: US/10/114,153

; CURRENT FILING DATE: 2002-08-06

; PRIOR APPLICATION NUMBER: 60/281086

; PRIOR FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: 60/281906

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/282020

; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/282930

; PRIOR FILING DATE: 2001-04-10

; PRIOR APPLICATION NUMBER: 60/283512

; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: 60/283444

; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: 60/283657

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283710

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; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 1
; LENGTH: 2813
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(2793)
US-10-114-153-1
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Query Match          95.7%; Score 1782.4; DB 15; Length 2813;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 68

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 128

Qy    121 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGGTGTCATCCTG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGGTGTCATCCTG 188

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 248

Qy    241 TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 TTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 308

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 368

Qy    361 ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 428

Qy    421 CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 CTGGGTTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 488

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 540
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Db    489 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC 548

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db	549	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	608
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	609	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	668
Qy	661	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	720
Db	669	CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC	728
Qy	721	TTTCCAGTGTGTGTCTTCTGGCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	729	TTTCCAGTGTGTGTCTTCTGGCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	788
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	789	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	848
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	900
Db	849	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC	908
Qy	901	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	909	CTGGTGCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	968
Qy	961	AAGGATCTGAAGCAAAAAACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	969	AAGGATCTGAAGCAAAAAACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1028
Qy	1021	TACTATGCTCTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080
Db	1029	TACTATGCTCTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1088
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1089	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1148
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1149	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1208
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1209	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1268
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1269	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1328
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1329	AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1388
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC	1440

Db 1389 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1448
 Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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 Db 1449 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1508
 Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA 1560
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1509 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCTAGCCTCCCCCTTGTGTGGCCACA 1568
 Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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 Db 1569 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1628
 Qy 1621 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1680
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1629 GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGGT 1688
 Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1689 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1748
 Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAACTGT 1784
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 Db 1749 GAAGACACATATGGGGAGTTGGAATTCAGAATGATGAACTGT 1792

RESULT 10

US-10-114-153-3

; Sequence 3, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Shenoy, Suresh

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter

; APPLICANT: Smithson, Glennnda

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gerlach, Valerie

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; APPLICANT: Li, Li

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Tchernev, Velizar

; APPLICANT: Gangolli, Esha

; APPLICANT: Vernet, Corine

; APPLICANT: Spytek, Kimberly

; APPLICANT: Malyankar, Uriel

; APPLICANT: Patturajan, Meera

; APPLICANT: Miller, Charles

; APPLICANT: Taupier, Raymond J. Jr.

; APPLICANT: Heyes, Melvyn

; APPLICANT: Ju, Jingfang

; APPLICANT: Peyman, John

; APPLICANT: Catterton, Elina

; APPLICANT: MacDougall, John

```

; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 3
; LENGTH: 2840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(2838)
US-10-114-153-3

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Query Match          95.7%; Score 1782.4; DB 15; Length 2840;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db      63 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 122

Qy      61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      123 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 182

Qy      121 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      183 ACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAGGGTGTATCCTG 242

Qy      181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

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Db	243	 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT	302
Qy	241	TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	303	 TTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	362
Qy	301	TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	360
Db	363	 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA	422
Qy	361	ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	420
Db	423	 ACCAGCACAAACCACTATTTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC	482
Qy	421	CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	480
Db	483	 CTGGGTTCCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTT	542
Qy	481	ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	543	 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATC	602
Qy	541	ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	600
Db	603	 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA	662
Qy	601	CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	660
Db	663	 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT	722
Qy	661	CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	720
Db	723	 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCCTCCTCACTCTCTTCTTC	782
Qy	721	TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	780
Db	783	 TTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC	842
Qy	781	ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	840
Db	843	 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC	902
Qy	841	CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCTATTTTCTAGATGGGAAAC	900
Db	903	 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCTATTTTCTAGATGGGAAAC	962
Qy	901	CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	963	 CTGGTGCCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC	1022
Qy	961	AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1020
Db	1023	 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT	1082
Qy	1021	TACTATGCTCTTTCCCAACAAGAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT	1080

Db	1083	TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT	1142
Qy	1081	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1140
Db	1143	ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC	1202
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1200
Db	1203	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT	1262
Qy	1201	GACCCATGTTCTTACCAGTGCCTGGGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1260
Db	1263	GACCCATGTTCTTACCAGTGCCTGGGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG	1322
Qy	1261	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1320
Db	1323	AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC	1382
Qy	1321	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1380
Db	1383	AATGCAGGGGCTGACTATGAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACC	1442
Qy	1381	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGAAGGAGGATGAACACTTC	1440
Db	1443	CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTGAAGGAGGATGAACACTTC	1502
Qy	1441	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1500
Db	1503	TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA	1562
Qy	1501	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCTTGTGTGGCCACA	1560
Db	1563	GCAATATTCAACAGTCTTCCCTTGCCCTCGGGCTGTCCTAGCCTCCCTTGTGTGGCCACA	1622
Qy	1561	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1623	GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT	1682
Qy	1621	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1680
Db	1683	GTCAGTGAGAGTATTGGTGTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGT	1742
Qy	1681	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1740
Db	1743	ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT	1802
Qy	1741	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT	1784
Db	1803	GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT	1846

RESULT 11

US-10-114-153-5

; Sequence 5, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennnda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 5
; LENGTH: 2685

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Qy	806	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	865
Db	722	AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG	781
Qy	866	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG	925
Db	782	GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG	841
Qy	926	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	985
Db	842	TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG	901
Qy	986	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCACCAACAGA	1045
Db	902	AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCACCAACAGA	961
Qy	1046	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1105
Db	962	AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC	1021
Qy	1106	TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG	1165
Db	1022	TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG	1081
Qy	1166	ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1225
Db	1082	ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG	1141
Qy	1226	AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA	1285
Db	1142	AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA	1201
Qy	1286	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1345
Db	1202	TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA	1261
Qy	1346	CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1405
Db	1262	CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA	1321
Qy	1406	TTGATGACGACATTTTGTAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1465
Db	1322	TTGATGACGACATTTTGTAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA	1381
Qy	1466	TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1525
Db	1382	TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC	1441
Qy	1526	CTCGGGCTGTCCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1585
Db	1442	CTCGGGCTGTCCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG	1501
Qy	1586	CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG	1645
Db	1502	CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG	1561

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Qy      1646 AGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGTACAGTCATCGTCCCCTTTAGGACAG 1705
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Db      1562 AGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGTACAGTCATCGTCCCCTTTAGGACAG 1621

Qy      1706 TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT 1765
          |||
Db      1622 TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT 1681

Qy      1766 TCAAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCC 1825
          |||
Db      1682 TCAAGAATGATGAAAC----TGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAA 1737

Qy      1826 AAGAGGATAGCAGAGA 1841
          |
Db      1738 TACGAAAGGCAAGAGA 1753

```

RESULT 12

US-10-029-386-20265

; Sequence 20265, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES

USEFUL FOR GENE

; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

; FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 20265

; LENGTH: 823

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AL160191.1

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

; OTHER INFORMATION: SWISSPROT HIT: P57103, EVALUE 0.00e+00

; OTHER INFORMATION: EST_HUMAN HIT: BI913344.1, EVALUE 0.00e+00

; OTHER INFORMATION: NT HIT: gi15147253, EVALUE 0.00e+00

US-10-029-386-20265

Query Match 44.1%; Score 821.4; DB 15; Length 823;

Best Local Similarity 99.9%; Pred. No. 1.6e-259;

Matches 822; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      432 TGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTCATTGCTGGTGA 491
          |||
Db      1   TGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTTCATTGCTGGTGA 60

Qy      492 TCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCAT 551

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Db	61	TCTGGGACCTTCTACCATTTGTAGGGAGTGCAGCCTTCAACATGTTTCATCATCATTGGCAT	120
Qy	552	CTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTT	611
Db	121	CTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTT	180
Qy	612	CATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTT	671
Db	181	CATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTT	240
Qy	672	CTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTG	731
Db	241	CTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTG	300
Qy	732	TGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAA	791
Db	301	TGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAA	360
Qy	792	GTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGG	851
Db	361	GTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGG	420
Qy	852	CATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCT	911
Db	421	CATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCT	480
Qy	912	GGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAA	971
Db	481	GGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAA	540
Qy	972	GCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCT	1031
Db	541	GCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCT	600
Qy	1032	TTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGG	1091
Db	601	TTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGG	660
Qy	1092	TGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAG	1151
Db	661	TGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAG	720
Qy	1152	CGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTC	1211
Db	721	CGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTC	780
Qy	1212	TTACCAAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTG	1254
Db	781	TTACCAAGTGCCTGGAGAAGTGTGGGGCTGTACTCCTGACAGTG	823

RESULT 13

US-09-901-419-1

; Sequence 1, Application US/09901419

; Patent No. US20020069421A1

; GENERAL INFORMATION:

```
; APPLICANT: The Curators of the University of Missouri
; TITLE OF INVENTION: LARGE SCALE EXPRESSION AND PURIFICATION OF RECOMBINANT
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: UMO1531.1
; CURRENT APPLICATION NUMBER: US/09/901,419
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/218,125
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4087
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (268)..(3180)
; NAME/KEY: sig_peptide
; LOCATION: (268)..(363)
; NAME/KEY: misc_feature
; LOCATION: (3178)
; OTHER INFORMATION: A Poly (H) affinity tag comprising 6 His residues
; OTHER INFORMATION: have been inserted at the C-Terminus end of the
; OTHER INFORMATION: coding region of the protein
US-09-901-419-1
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Query Match          43.5%; Score 810.6; DB 9; Length 4087;
Best Local Similarity 68.5%; Pred. No. 1.6e-255;
Matches 1211; Conservative 0; Mismatches 519; Indels 39; Gaps 5;
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Qy      46 TTTGGGCTGGTTACCTTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCA 105
      |||  || | || | |||  || || | | | | | | |||
Db      307 TTTCACGTGATAGCCATGGTGGCTCTCTTGTTTTCCCATGTGGACCATATAAGTGCTGAG 366

Qy      106 GGGGACGTGCCAAGCACAGGGCAGAACAAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAG 165
      ||  || | | | ||| | | |||  ||| || || | ||| |||
Db      367 ACAGAAATGGAAGGAGAAGGCAACGAGACTGGCGAGTGTACTGGCTCCTATTACTGTAAG 426

Qy      166 GAGGGTGTTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCC 225
      |||| || || | || || ||| | || | || ||||| |||| |||| ||||
Db      427 AAGGGGGTGATTTTACCCATTTGGGAGCCCCAGGACCCTTCCTTTGGAGACAAAATTGCT 486

Qy      226 AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCT 285
      || | | ||| ||||| ||||| || | ||||| ||||| || || ||||| |||
Db      487 AGAGCGACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCAATCATTGCT 546

Qy      286 GACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAG 345
      ||||| ||||| | ||||| ||||| ||||| ||||| || | || || |||
Db      547 GACCGGTTTCATGTCCTCTATAGAAGTCATCACGTCTCAAGAGAAAGAAATCACCATAAAG 606

Qy      346 AAACCCAATGGAGAAACCAGCACAAACCACTATTCGGGTCTGGAATGAACTGTCTCCAAC 405
      ||||| ||||| ||||| || || || || | || ||||| || || |||||
Db      607 AAACCCAATGGAGAGACCACCAAGACAACCTGTGAGGATCTGGAATGAGACAGTGTC AAC 666

Qy      406 CTGACCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTG 465
      ||||| | ||||| ||||| || || ||||| ||||| ||||| || |||||
Db      667 CTGACCTTGATGGCCCTGGGGTCTTCAGCTCCAGAGATTCTCCTTTCAGTAATCGAGGTG 726
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Qy	466	TGTGGTTCATGGGTTTCATTGCTGGT	GATCTGGGACCTTCTACCATTTG	TAGGGAGTGCAGCC	525
Db	727	TGTGGCCATAACTTTCAC	TGCAGGAGACCTTGGCCCTAGC	CACCATCGTGGGGAGT	GCTGCA 786
Qy	526	TTCAACATGTTTCATCATCATTGGC	CATCTGTGTCTACGTGATCCCAG	ACGGAGAGACTCGC	585
Db	787	TTCAACATGTTTCATCATCATTGCC	CTTTGTGTGTATGTCGTCCCGG	ATGGGGAGACAAGG	846
Qy	586	AAGATCAAGCATCTACGAGTCTTCT	TTCATCACCGCTGCTTGGAGTAT	CTTTGCCTACATC	645
Db	847	AAGATCAAGCATCTGCGTGTGTTCT	TTGTGACAGCAGCATGGAGCAT	CTTTGCCTATACC	906
Qy	646	TGGCTCTATATGATTCTGGCAGTCT	TCTCCCCTGGTGTGGTCCAGGTT	TGGGAAGGCCTC	705
Db	907	TGGCTTTACATCATTTTGTCTGT	CAGCTCCCCTGGGGTCGTGGAG	GTCTGGGAAGGTTTG	966
Qy	706	CTCACTCTCTTCTTCTTTCCAGT	GTGTGTCCTTCTGGCCTGGGT	GGCAGATAAACGACTG	765
Db	967	CTTACTTTCTTCTTCTTTCCCAT	CTGCGTTGTGTTGCTTGGGT	GGCAGACAGGAGGCTT	1026
Qy	766	CTCTTCTACAAATACATGCACAAA	AGTACCGCACAGACAAACACCG	AGGAATTATCATA	825
Db	1027	CTGTTTTACAAGTATGTCTACA	AGAGGTATCGGGCTGGCAAGC	AGAGGGGAATGATTATT	1086
Qy	826	GAGACAGAGGGGTGACCACCC	-----TAAGGGCATTGAGAT	GGATGGGAAAATGATG	876
Db	1087	GAACACGAAGGAGACAGGCCAT	CTTCCAAGACAGAAATTGAAAT	GGATGGGAAAGTGGTC	1146
Qy	877	AATTCCCA-----TTTTCT	AGATGGGAACCTGGTGCCCT	TGGAAGGGAAG-----	921
Db	1147	AATTCCCATGTTGACAGTTTCT	TAGATGGAGCCCTGGTCTG	GAGGTTGATGAGAGGGAC	1206
Qy	922	---GAAGTGGATGAGTCCCGC	AGAGAGATGATCCGGATTCT	CAAGGATCTGAAGCAAAAA	978
Db	1207	CAAGATGATGAAGAAGCCAG	GCGAGAAATGGCTAGGATT	CTGAAGGAACCTCAAGCAGAAG	1266
Qy	979	CACCCAGAGAAGGACTTAGAT	CAGCTGGTGGAGATGGCCA	ATTACTATGCTCTTTCCAC	1038
Db	1267	CATCCAGAGAAGGAAATAG	AGCAATTAATAGAATTAG	CCAATTACCAAGTCTTAAGTCAG	1326
Qy	1039	CAACAGAAGAGCCGCGCCTT	CTACCGTATCCAAGCCACT	CGTATGATGACTGGTGCAGGC	1098
Db	1327	CAGCAAAAAAGTCGAGCGT	TTTACCGTATTCAAGCT	TACCGCCTGATGACCGGAGCAGGC	1386
Qy	1099	AATATCCTGAAGAAACAT	GCAGCAGAACCAAGCCA	AGAAGGCCTCCAGCATGAGCGAGGTG	1158
Db	1387	AACATTTTAAAGAGGCAT	GCAGCAGACCAAGCCAG	GAAAGCTGTCAGCATGCATGAGGTC	1446
Qy	1159	CACACCGATGAGCCTG---	AGGACTTTATTTCCAAGG	TCTTCTTTGACCCATGTTCTTAC	1215
Db	1447	AACACGGAAGTGGCTG	AAAATGACCCTGT	CAGTAAGATCTTCTTTGAACAAGGGACATAT	1506
Qy	1216	CAGTGCCTGGAGAACTGT	GGGGCTGTACTCCTGACAGT	GGTGAGGAAAGGGGGAGACATG	1275
Db	1507	CAGTGTCTGGAGAACTGT	GGCACAGTAGCCCTGAC	CATTATCCGCAGAGGTGGTGATTG	1566

Db	133	GAAATGGAAGGAGAAGGAAATGAAACTGGTGAATGTACTGGATCATATTACTGTAAGAAA	192
Qy	169	GGTGTTCATCCTGCCAATCTGGTACCCGGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGG	228
Db	193	GGGGTGATTTTGGCCATTTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAATTGCTAGA	252
Qy	229	GTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCCTTGGGGTGTCCATCATTGCTGAC	288
Db	253	GCTACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT	312
Qy	289	CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAA	348
Db	313	CGGTTTCATGTCTCTATAGAAGTCATCACATCTCAAGAAAAAGAAATAACCATAAAGAAA	372
Qy	349	CCCAATGGAGAAACCAGCACAACTTATTCGGGTCTGGAATGAAACTGTCTCCAACCTG	408
Db	373	CCCAATGGAGAGACCACCAAGACAACCTGTGAGGATCTGGAATGAAACAGTTTCTAACCTG	432
Qy	409	ACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT	468
Db	433	ACCTTGATGGCCCTGGGATCTTCTGCTCCTGAGATTCTCCTTTCAGTAATTGAAGTGTGT	492
Qy	469	GGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTC	528
Db	493	GGCCATAACTTCACTGCAGGAGACCTCGGTCTAGCACCATCGTGGGAAGTGTGCATTC	552
Qy	529	AACATGTTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAG	588
Db	553	AATATGTTTCATCATTATTGCACTCTGTGTTTATGTGGTGCCTGACGGAGAGACAAGGAAG	612
Qy	589	ATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGG	648
Db	613	ATTAAGCATTTGCGTGTCTTCTTTGTGACAGCAGCCTGGAGCATCTTTGCCTACACCTGG	672
Qy	649	CTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTC	708
Db	673	CTTTACATTATTTTGTCTGTCTATCTCCTGGTGTGTGGAGGTCTGGGAAGGTTTGCTT	732
Qy	709	ACTCTCTTCTTCTTTCCAGTGTGTGTCTTCTGGCCTGGGTGGCAGATAAACGACTGCTC	768
Db	733	ACTTTCTTCTTCTTTCCATCTGTGTTGTGTTTCGCTTGGGTAGCGGATAGGAGACTTCTG	792
Qy	769	TTCTACAAATACATGCACAAAAAGTACCGCACAGACAAAACCCGAGGAATTATCATAGAG	828
Db	793	TTTTACAAGTATGTCTACAAGAGGTATCGAGCTGGCAAGCAGAGGGGGATGATTATTGAA	852
Qy	829	ACAGAGGGTGACCACCC-----TAAGGGCATTGAGATGGATGGGAAAATGATGAAT	879
Db	853	CATGAAGGAGACAGGCCATCTTCTAAGACTGAAATTGAAATGGACGGGAAAGTGGTCAAT	912
Qy	880	TCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAG-----	921
Db	913	TCTCATGTTGAAAATTTCTTAGATGGTGTCTGTTTCTGGAGGTGGATGAGAGGGACCAA	972
Qy	922	GAAGTGGATGAGTCCCGCAGAGAGATGATCCGATTCTCAAGGATCTGAAGCAAAAACAC	981
Db	973	GATGATGAAGAAGCTAGGCGAGAAATGGCTAGGATTCTGAAGGAACTTAAGCAGAAGCAT	1032

Qy	982	CCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCAACAA	1041
Db	1033		
Qy	1042	CCAGATAAAGAAATAGAGCAATTAATAGAATTAGCTAACTACCAAGTCCTAAGTCAGCAG	1092
Qy	1042	CAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAAT	1101
Db	1093		
Qy	1093	CAAAAAAGTAGAGCATTTTATCGCATTCAAGCTACTCGCCTCATGACTGGAGCTGGCAAC	1152
Qy	1102	ATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCAC	1161
Db	1153		
Qy	1153	ATTTTAAAGAGGCATGCAGCTGACCAAGCAAGGAAGGCTGTCTGAGCATGCACGAGGTCAAC	1212
Qy	1162	ACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG	1218
Db	1213		
Qy	1213	ACTGAAGTGACTGAAAATGACCCGTGTAGTAAGATCTTCTTTGAACAAGGGACATATCAG	1272
Qy	1219	TGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGAGACATGTCA	1278
Db	1273		
Qy	1273	TGTCTGGAGAACTGTGGTACTGTGGCCCTTACCATTATCCGCAGAGGTGGTGATTTGACT	1332
Qy	1279	AAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTAT	1338
Db	1333		
Qy	1333	AACACTGTGTTTGTGACTTCAGAACAGAGGATGGCACAGCAAATGCTGGGTCTGATTAT	1392
Qy	1339	GAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCCTCCGTG	1398
Db	1393		
Qy	1393	GAATTTACTGAAGGAACGTGGTGTTTAAGCCTGGTGATACCAGAAGGAAATCAGAGTG	1452
Qy	1399	GGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAAT	1458
Db	1453		
Qy	1453	GGTATCATAGATGATGATATCTTTGAGGAGGATGAAAATTCCTTGTGCATCTCAGCAAT	1512
Qy	1459	GTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTT	1518
Db	1513		
Qy	1513	GTCAAAGTATCTTCTGAAGCTTCAGAAGATGGCATACTGGAAGC-----CAATCAT	1563
Qy	1519	CCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGATGAT	1578
Db	1564		
Qy	1564	GTTTCTACACTTGCTTGCCTCGGATCTCCCTCCACTGCCACTGTAACATTTTTGATGAT	1623
Qy	1579	GACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGT	1638
Db	1624		
Qy	1624	GACCACGCAGGCATTTTTACTTTTGAGGAACCTGTGACTCATGTGAGTGAGAGCATTTGGC	1683
Qy	1639	GTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGTACAGTCATCGTCCCCTTT	1698
Db	1684		
Qy	1684	ATCATGGAGGTGAAAGTATTGAGAACATCTGGAGCTCGAGAAATGTTATCGTTCCATAT	1743
Qy	1699	AGGACAGTAGAAGGGACAGCCAAGGTTGGCGGTGAGGACTTTGAAGACACATATGGGGAG	1758
Db	1744		
Qy	1744	AAAACCATCGAAGGGACTGCCAGAGGTGGAGGGGAGGATTTGAGGACACTTGTGGAGAG	1803
Qy	1759	TTGGAATTCAAGAATGATGAACTGTAT	1786
Db	1804		
Qy	1804	CTCGAATTCCAGAATGATGAAATTGTGT	1831

RESULT 15

US-10-062-674-1648

; Sequence 1648, Application US/10062674

; Publication No. US20040005559A1

; GENERAL INFORMATION:

; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.

; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS

; FILE REFERENCE: PA-0026-1 CIP

; CURRENT APPLICATION NUMBER: US/10/062,674

; CURRENT FILING DATE: 2002-01-30

; PRIOR APPLICATION NUMBER: US 09/625,102

; PRIOR FILING DATE: 2000-07-24

; NUMBER OF SEQ ID NOS: 2217

; SOFTWARE: PERL Program

; SEQ ID NO 1648

; LENGTH: 6106

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20040005559A1 221501.2

US-10-062-674-1648

Query Match 42.0%; Score 783.2; DB 16; Length 6106;
Best Local Similarity 68.2%; Pred. No. 2.3e-246;
Matches 1164; Conservative 0; Mismatches 503; Indels 39; Gaps 4;

Qy	109	GACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTTCAGGGTCATCGGACTGCAAGGAG	168
Db	192	GAAATGGAAGGAGAAGGAAATGAACTGGTGAATGTACTGGATCATATTACTGTAAGAAA	251
Qy	169	GGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGG	228
Db	252	GGGGTGATTTTGGCCATTTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAATTGCTAGA	311
Qy	229	GTCATTGTCTATTTTGTGGCCCTGATATACATGTTTCCTTGGGGTGTCCATCATTGCTGAC	288
Db	312	GCTACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT	371
Qy	289	CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAA	348
Db	372	CGGTCATGTCTCTATAGAAGTCATCACATCTCAAAAAAAGAAATAACCATAAAGAAA	431
Qy	349	CCCAATGGAGAAACCAGCACAACTACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTG	408
Db	432	CCCAATGGAGAGACCACCAAGACAACCTGTGAGGATCTGGAATGAAACAGTTTCTAACCTG	491
Qy	409	ACCCTTATGGCCCTGGGTTCTCTGCTCCTGAGATACTCTCTCTTTAATTGAGGTGTGT	468
Db	492	ACCTTGATGGCCCTGGGATCTTCTGCTCCTGAGATTCTCTTTTCAGTAATTGAAGTGTGT	551
Qy	469	GGTCATGGGTTTCATTGCTGGTGATCTGGGACCTTCTACCATTTAGGGAGTGCAGCCTTC	528
Db	552	GGCCATAACTTCACTGCAGGAGACCTCGGTCTAGCACCATCGTGGGAAGTGTGCTGCATTC	611
Qy	529	AACATGTTTCATCATCATTTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAG	588

Db	612	AATATGTTTCATCATTATTGCACTCTGTGTTTATGTGGTGCCTGACGGAGAGACAAGGAAG	671
Qy	589	ATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGG	648
Db	672	ATTAAGCATTTGCGTGTCTTCTTGTGACAGCAGCCTGGAGCATCTTTGCCTACACCTGG	731
Qy	649	CTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTC	708
Db	732	CTTTACATTATTTTGTCTGTCTATCTCCTGGTGTGTGGAGGTCTGGGAAGGTTTGCTT	791
Qy	709	ACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTC	768
Db	792	ACTTTCTTCTTCTTTCCCATCTGTGTTGTGTTTCGCTTGGGTAGCGGATAGGAGACTTCTG	851
Qy	769	TTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAG	828
Db	852	TTTTACAAGTATGTCTACAAGAGGTATCGAGCTGGCAAGCAGAGGGGGATGATTATTGAA	911
Qy	829	ACAGAGGGTGACCACCC-----TAAGGGCATTGAGATGGATGGGAAAATGATGAAT	879
Db	912	CATGAAGGAGACAGGCCATCTTCTAAGACTGAAATTGAAATGGACGGGAAAGTGGTCAAT	971
Qy	880	TCCCATTTTCTAGATGGGAACCTGGTGCCCTGGAAGGGAAG-----	921
Db	972	TCTCATGTTGAAAATTTCTTAGATGGTGCTCTGGTTCTGGAGGTGGATGAGAGGGACCAA	1031
Qy	922	GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACAC	981
Db	1032	GATGATGAAGAAGCTAGGCGAGAAATGGCTAGGATTCTGAAGGAACTTAAGCAGAAGCAT	1091
Qy	982	CCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAA	1041
Db	1092	CCAGATAAAGAAATAGAGCAATTAAATAGAATTAGCTAACTACCAAGTCCTAAGTCAGCAG	1151
Qy	1042	CAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAAT	1101
Db	1152	CAAAAAAGTAGAGCATTATTCGCATTCAAGCTACTCGCCTCATGACTGGAGCTGGCAAC	1211
Qy	1102	ATCCTGAAGAAACATGCAGCAGAACAAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCAC	1161
Db	1212	ATTTTAAAGAGGCATGCAGCTGACCAAGCAAGGAAGGCTGTGAGCATGCACGAGGTCAAC	1271
Qy	1162	ACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG	1218
Db	1272	ACTGAAGTGACTGAAAATGACCCTGTTAGTAAGATCTTCTTTGAACAAGGGACATATCAG	1331
Qy	1219	TGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCA	1278
Db	1332	TGTCTGGAGAACTGTGGTACTGTGGCCCTTACCATTATCCGCAGAGGTGGTGATTGACT	1391
Qy	1279	AAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTAT	1338
Db	1392	AACACTGTGTTTGTGACTTCAGAACAGAGGATGGCACAGCAAATGCTGGGTCTGATTAT	1451
Qy	1339	GAGTTCACAGAGGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTG	1398

Db	1452	GAATTTACTGAAGGAAGCTGTGGTGT'TTAAGCCTGGTGATACCCAGAAGGAAATCAGAGTG	1511
Qy	1399	GGCATAATTGATGACGACATTTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAAT	1458
Db	1512	GGTATCATAGATGATGATATCTTTGAGGAGGATGAAAATTCCTTGTGCATCTCAGCAAT	1571
Qy	1459	GTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTT	1518
Db	1572	GTCAAAGTATCTTCTGAAGCTTCAGAAGATGGCATACTGGAAGC-----CAATCAT	1622
Qy	1519	CCCTTGCCCTCGGGCTGTCCTAGCCTCCCCTTGTTGGCCACAGTTACCATCTTGGATGAT	1578
Db	1623	GTTTCTACACTTGCTTGCCTCGGATCTCCCTCCACTGCCACTGTAACATTTTTTGATGAT	1682
Qy	1579	GACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTTCATGTCAGTGAGAGTATTGGT	1638
Db	1683	GACCACGCAGGCATTTTTACTTTTGAGGAACCTGTGACTCATGTGAGTGAGAGCATTGGC	1742
Qy	1639	GTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCCGGGTACAGTCATCGTCCCCTTT	1698
Db	1743	ATCATGGAGGTGAAAGTATTGAGAACATCTGGAGCTCGAGGAAATGTTATCGTTCCATAT	1802
Qy	1699	AGGACAGTAGAAGGGACAGCCAAGGTTGGCGGTGAGGACTTTGAAGACACATATGGGGAG	1758
Db	1803	AAAACCATCGAAGGGACTGCCAGAGGTGGAGGGGAGGATTTGAGGACACTTGTGGAGAG	1862
Qy	1759	TTGGAATTCAAGAATGATGAACTGT	1784
Db	1863	CTCGAATTCCAGAATGATGAAATTGT	1888

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Job time : 760.008 secs